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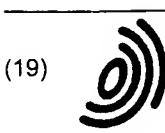
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(54) ENZYMATISCHE VERFAHREN DASS ENZYME DIE AN DER ZELLWAND EINER EUKARYONTISCHEN MIKROBIELLEN ZELLE DURCH SCHAFFUNG EINES FUSIONSPROTEINS IMMOBILISIERT WURDEN VERWENDET.

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PROCEDE ENZYMATIQUE UTILISANT DES ENZYMES IMMOBILISEES SUR LA PAROI CELLULAIRE D'UNE CELLULE MICROBIENNE EUCHARIOOTE EN PRODUISANT UNE PROTEINE DE FUSION

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Description

[0001] The present invention is in the field of conversion processes using immobilized enzymes, produced by genetic engineering.

5

Background of the invention

[0002] In the detergent, personal care and food products industry there is a strong trend towards natural ingredients of these products and to environmentally acceptable production processes. Enzymic conversions are very important for fulfilling these consumer demands, as these processes can be completely natural. Moreover enzymic processes are very specific and consequently will produce minimum amounts of waste products. Such processes can be carried out in water at mild temperatures and atmospheric pressure. However enzymic processes based on free enzymes are either quite expensive due to the loss of enzymes or require expensive equipment, like ultra-membrane systems to entrap the enzyme.

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[0003] Alternatively enzymes can be immobilized either physically or chemically. The latter method has often the disadvantage that coupling is carried out using non-natural chemicals and in processes that are not attractive from an environmental point of view. Moreover chemical modification of enzymes is nearly always not very specific, which means that coupling can affect the activity of the enzyme negatively.

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[0004] Physical immobilization can comply with consumer demands, however also physical immobilization may affect the activity of the enzyme in a negative way. Moreover, a physically immobilized enzyme is in equilibrium with free enzyme, which means that in continuous reactors, according to the laws of thermodynamics, substantial losses of enzyme are unavoidable.

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[0005] There are a few publications on immobilization of enzymes to microbial cells (see reference 1). The present invention provides a method for immobilizing enzymes to cell walls of microbial cells in a very precise way. Additionally, the immobilization does not require any chemical or physical coupling step and is very efficient.

25

[0006] Some extracellular proteins are known to have special functions which they can perform only if they remain bound to the cell wall of the host cell. Often this type of protein has a long C-terminal part that anchors it in the cell wall. These C-terminal parts have very special amino acid sequences. A typical example is anchoring via C-terminal sequences enriched in proline (see reference 2). Another mechanism to anchor proteins in cell walls is that the protein has a glycosyl-phosphatidyl-inositol (GPI) anchor (see reference 3) and that the C-terminal part of the protein contains a substantial number of potential serine and threonine glycosylation sites.

30

[0007] O-Glycosylation of these sites gives a rod-like conformation to the C-terminal part of these proteins. Another feature of these manno-proteins is that they seem to be linked to the glucan in the cell wall of lower eukaryotes, as they cannot be extracted from the cell wall with SDS, but can be liberated by glucanase treatment.

35

Summary of the invention

[0008] The invention relates to use of a lower eukaryote selected from the group consisting of yeasts and fungi containing an expressible first polynucleotide comprising a structural gene encoding a protein providing catalytic activity, said protein being immobilised at the exterior of the cell wall of said lower eukaryote, and at least part of a gene encoding an anchoring protein capable of anchoring in the cell wall of said lower eukaryote, said part encoding at least the anchoring part of said anchoring protein, which anchoring part is derivable from the C-terminal half of said anchoring protein, said first polynucleotide being present in either a vector or in a chromosome of said lower eukaryote, for carrying out an enzymatic process, by contacting a substrate for the protein providing catalytic activity, with the lower eukaryote.

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[0009] The invention relates to the use of a recombinant polynucleotide comprising a structural gene encoding a protein providing catalytic activity and at least a part of a gene encoding a protein capable of anchoring in a eukaryotic or prokaryotic cell wall, said part encoding at least the C-terminal part of said anchoring protein for carrying out an enzymatic process. Preferably the polynucleotide further comprises a sequence encoding a signal peptide ensuring secretion of the expression product of the polynucleotide. Such signal peptide can be derived from a glycosyl-phosphatidyl-inositol (GPI) anchoring protein, α -factor, α -agglutinin, invertase or inulinase, α -amylase of *Bacillus*, or a proteinase of lactic acid bacteria. The DNA sequence encoding a protein capable of anchoring in the cell wall can encode α -agglutinin, AGA1, FLO1 or the Major Cell Wall Protein of lower eukaryotes, or a proteinase of lactic acid bacteria. The recombinant polynucleotide is operably linked to a promoter, preferably an inducible promoter. The DNA sequence encoding a protein providing catalytic activity can encode a hydrolytic enzyme, e.g. a lipase, or an oxidoreductase, e.g. an oxidase. Another embodiment of the invention relates to a recombinant vector comprising a polynucleotide as described above. If such vector contains a DNA sequence encoding a protein providing catalytic activity, which protein exhibits said catalytic activity when present in a multimeric form, said vector can further comprise a second polynucleotide comprising a structural gene encoding the same protein providing catalytic activity combined with a sequence

encoding a signal peptide ensuring secretion of the expression product of said second polynucleotide, said second polynucleotide being operably linked to a regulatable promoter, preferably an inducible or repressible promoter.

[0010] If the protein providing catalytic activity exhibits said catalytic activity when present in a multimeric form, said host cell or microorganism can further comprise a second polynucleotide comprising a structural gene encoding the same protein providing catalytic activity combined with a sequence encoding a signal peptide ensuring secretion of the expression product of said second polynucleotide, said second polynucleotide being operably linked to a regulatable promoter, preferably an inducible or repressible promoter, and said second polynucleotide being present either in another vector or in the chromosome of said microorganism. Preferably the host cell or microorganism has at least one of said polynucleotides integrated in its chromosome. As a result of culturing such host cell or microorganism the invention provides a host cell, preferably a microorganism, having a protein as described above immobilized on its cell wall. The host cell or microorganism can be a lower eukaryote, in particular a yeast.

[0011] The invention provides a process for carrying out an enzymatic process by using an immobilized catalytically active protein, wherein a substrate for said catalytically active protein is contacted with a host cell or microorganism according to the invention.

15

Brief Description of the Figures

[0012]

20 Figure 1: DNA sequence of the 6057 bp *Hind*III fragment containing the complete AG α 1 gene of *S. cerevisiae* (see SEQ ID NO: 1 and 2). The position of the unique *Nhe*I site and the *Hind*III site used for the described constructions is specified in the header.

25 Figure 2: Schematic presentation of the construction of pUR2969. The restriction sites for endonucleases used are shown. Abbreviations used: AG-alpha-1: Gene expressing α -agglutinin from *S. cerevisiae*

amp: β -lactamase resistance gene

PGKp: phosphoglyceratekinase promoter

PGKt: terminator of the same gene.

30 Figure 3: α -Galactosidase activity of *S. cerevisiae* MT302/1C cells and culture fluid transformed with pSY13 during batch culture:

A: U/l α -galactosidase per time; the OD₅₃₀ is also shown

B: α -galactosidase activity of free and bond enzyme expressed in U/OD₅₃₀.

35 Figure 4: α -Galactosidase activity of *S. cerevisiae* MT302/1C cells and culture fluid transformed with pUR2969 during batch culture:

A: U/l α -galactosidase per time; the OD₅₃₀ is also shown

B: α -galactosidase activity of free and bond enzyme expressed in U/OD₅₃₀.

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Figure 5: Western analysis with anti α -galactosidase serum of extracellular fractions of cells of exponential phase (OD₅₃₀=2). The analyzed fractions are equivalent to 4 mg cell walls, (fresh weight):

A: MT302/1C expressing α -galactosidase,

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lane 1, growth medium

lane 2, SDS extract of isolated cell walls

lane 3, glucanase extract of SDS extracted cell walls;

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B: MT302/1C expressing α -Gal-AG α 1 fusion protein,

lane 1, growth medium

lane 2, SDS extract of isolated cell walls

lane 3, glucanase extract of SDS-extracted cell walls

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lane 4: Endo-H treated glucanase extract.

Figure 6: Immunofluorescent labelling (anti α -galactosidase) of MT302/1C cells in the exponential phase (OD₅₃₀=2) expressing the α -Gal- α -agglutinin fusion protein.

Phase micrograph of intact cells A: overview B: detail.

Figure 7: Schematic presentation of the construction of pUR2970A, pUR2971A, pUR2972A, and pUR2973. The restriction sites for endonucleases used are indicated in the figure. PCR oligonucleotide sequences are mentioned in the text.

Abbreviations used:
 a-AGG=AGa1: Gene expressing α -agglutinin from *S. cerevisiae*
 amp: β -lactamase resistance gene Pgal7=GAL7: GAL7 promoter
 lipolase: lipase gene of *Humicola* invSS: SUC2 signal sequence
 a-MF: prepro- α -mating factor sequence a-gal: α -galactosidase gene
 LEU2d: truncated promoter of *LEU2* gene;
 LEU2 : *LEU2* gene with complete promoter sequence.

Figure 8: DNA sequence of a fragment containing the complete coding sequence of lipase B of *Geotrichum candidum* strain 335426 (see SEQ ID NO: 11 and 12). The sequence of the mature lipase B starts at nucleotide 97 of the given sequence. The coding sequence starts at nucleotide 40 (ATG).

Figure 9: Schematic presentation of the construction of pUR2975 and pUR2976. The restriction sites for endonucleases used are shown. Abbreviations used:

a-AGG: Gene expressing α -agglutinin from *S. cerevisiae*
 amp: β -lactamase resistance gene Pgal7 = GAL7: GAL7 promoter
 invSS: SUC2 signal sequence a-MF: prepro- α -mating factor sequence
 LEU2d: truncated promoter *LEU2* gene lipolase: lipase gene of *Humicola*
 lipaseB: lipaseB gene of *Geotrichum candidum*.

Figure 10: Schematic presentation of the construction of pUR2981 and pUR2982. The restriction sites for endonucleases used are shown. Abbreviations used:

a-AGG=AG-alpha 1: Gene expressing α -agglutinin from *S. cerevisiae*
 mucor lipase: lipase gene of *Rhizomucor miehei* 2u: 2 μ m sequence
 Pgal7=GAL7: GAL7 promoter invSS: SUC2 signal sequence
 a-MF: prepro- α -mating factor sequence lipolase: lipase gene of *Humicola*
 amp: β -lactamase resistance gene; LEU2d: truncated promoter *LEU2* gene
 LEU2 : *LEU2* gene with complete promoter sequence.

Figure 11: DNA sequence (2685 bases) of the 894 amino acids coding part of the *FLO1* gene (see SEQ ID NO: 21 and 22), the given sequence starts with the codon for the first amino acid and ends with the stop codon.

Figure 12: Schematic presentation of plasmid pUR2990. Some restriction sites for endonucleases relevant for the given cloning procedure are shown.

Figure 13: Schematic presentation of plasmid pUR7034.

Figure 14: Schematic presentation of plasmid pUR2972B.

Figure 15: Immunofluorescent labelling (anti-lipolase) of SU10 cells in the exponential phase ($OD_{530}=0.5$) expressing the lipolase-/a-agglutinin fusion protein.

A: phase micrograph B: matching fluorescent micrograph

40 Detailed description of the invention

[0013] The present invention provides a method for immobilizing an enzyme, comprising immobilizing the enzyme or a functional part thereof to the cell wall of a host cell, preferably a microbial cell, using recombinant DNA techniques. In particular, the C-terminal part of a protein that ensures anchoring in the cell wall is linked to an enzyme or the functional part of an enzyme, in such a way that the enzyme is localized on or just above the cell surface. In this way immobilized enzymes are obtained on the surface of cells. The linkage is performed at gene level and is characterized in that the structural gene coding for the enzyme is coupled to at least part of a gene encoding an anchor-protein in such a way that in the expression product the enzyme is coupled at its C-terminal end to the C-terminal part of an anchor-protein. The chimeric enzyme is preferably preceded by a signal sequence that ensures efficient secretion of the chimeric protein.

[0014] Thus the invention relates to a recombinant polynucleotide comprising a structural gene encoding a protein providing catalytic activity and at least a part of a gene encoding a protein capable of anchoring in a eukaryotic or prokaryotic cell wall, said part encoding at least the C-terminal part of said anchoring protein. The length of the C-terminal part of the anchoring protein may vary. Although the entire structural protein could be used, it is preferred that only a part is used, leading to a more efficient exposure of the enzyme protein in the medium surrounding the cell. The anchoring part of the anchoring protein should preferably be entirely present. As an example, about the C-terminal half of the anchoring protein could be used.

[0015] Preferably, the polynucleotide further comprises a sequence encoding a signal peptide ensuring secretion of

the expression product of the polynucleotide. The signal peptide can be derived from a GPI anchoring protein, α -factor, α -agglutinin, invertase or inulinase, α -amylase of *Bacillus*, or a proteinase of lactic acid bacteria.

[0016] The protein capable of anchoring in the cell wall is preferably selected from the group of α -agglutinin, AGA1, FLO1 (flocculation protein) or the Major Cell Wall Protein of lower eukaryotes, or a proteinase of lactic acid bacteria.

5 The polynucleotide of the invention is preferably operably linked to a promoter, preferably a regulatable promoter, especially an inducible promoter.

[0017] The invention also relates to a recombinant vector containing the polynucleotide as described above, and to a host cell containing this polynucleotide, or this vector.

10 [0018] In a particular case, wherein the protein providing catalytic activity exhibits said catalytic activity when present in a multimeric form, such as may be the case with oxidoreductases, dimerisation or multimerisation of the monomers might be a prerequisite for activity. The vector and/or the host cell can then further comprise a second polynucleotide comprising a structural gene encoding the same protein providing catalytic activity combined with a sequence encoding a signal peptide ensuring secretion of the expression product of said second polynucleotide, said second polynucleotide being operably linked to a regulatable promoter, preferably an inducible or repressible promoter. Expression and secretion of the second polynucleotide after expression and secretion of the first polynucleotide will then result in the formation of an active multimer on the exterior of the cell wall.

15 [0019] The host cell or microorganism preferably contains the polynucleotide described above, or at least one of said polynucleotides in the case of a combination, integrated in its chromosome.

20 [0020] The present invention relates to lower eukaryotes like yeasts that have very stable cell walls and have proteins that are known to be anchored in the cell wall, e.g. α -agglutinin or the product of gene *FLO1*. Suitable yeasts belong to the genera *Candida*, *Debaryomyces*, *Hansenula*, *Kluyveromyces*, *Pichia* and *Saccharomyces*.

25 [0021] Also fungi, especially *Aspergillus*, *Penicillium* and *Rhizopus* can be used. For certain applications also prokaryotes are applicable.

[0022] For yeasts the present invention deals in particular with genes encoding chimeric enzymes consisting of:

- 25 a. the signal sequence e.g. derived from the α -factor-, the invertase-, the α -agglutinin- or the inulinase genes;
 b. structural genes encoding hydrolytic enzymes such as α -galactosidase, proteases, peptidases, pectinases, pectylesterase, rhamnogalacturonase, esterases and lipases, or non-hydrolytic enzymes such as oxidases; and
 c. the C-terminus of typically cell wall bound proteins such as α -agglutinin (see reference 4), AGA1 (see reference 5) and FLO1 (see the non-prior published reference 6).

30 [0023] The expression of these genes can be under the control of a constitutive promoter, but more preferred are regulatable, i.e. repressible or inducible promoters such as the *GAL7* promoter for *Saccharomyces*, or the inulinase promoter for *Kluyveromyces* or the methanol-oxidase promoter for *Hansenula*.

35 [0024] Preferably the constructs are made in such a way that the new genetic information is integrated in a stable way in the chromosome of the host cell.

[0025] The invention further relates to a host cell, in particular a microorganism, having the chimeric protein described above immobilized on its cell wall. It concerns the use of such microorganisms for carrying out an enzymatic process by contacting a substrate for the enzyme with the microorganism. Such a process may be carried out e.g. in a packed 40 column, wherein the microorganisms may be supported on solid particles, or in a stirred reactor. The reaction may be aqueous or non-aqueous. Where necessary, additives necessary for the performance of the enzyme, e.g. a co-factor, may be introduced in the reaction medium.

[0026] After repeated usage of the naturally immobilized enzyme system in processes, the performance of the system may decrease. This is caused either by physical denaturation or by chemical poisoning or detachment of the enzyme.

45 A particular feature of the present invention is that after usage the system can be recovered from the reaction medium by simple centrifugation or membrane filtration techniques and that the thus collected cells can be transferred to a recovery medium in which the cells revive quickly and concomitantly produce the chimeric protein, thus ensuring that the surface of the cells will be covered by fully active immobilized enzyme. This regeneration process is simple and cheap and therefore will improve the economics of enzymic processes and may result in a much wider application of processes based on immobilized enzyme systems.

50 [0027] However, by no means the present invention is restricted to the reusability of the immobilized enzymes.

[0028] The invention will be illustrated by the following examples without the scope of the invention being limited thereto.

55 **EXAMPLE 1 Immobilized α -galactosidase/ α -agglutinin on the surface of *S. cerevisiae*.**

[0029] The gene encoding α -agglutinin has been described by Lipke *et al.* (see reference 4). The sequence of a 6057 bp *Hind*III insert in pTZ18R, containing the whole AGa1 gene is given in Figure 1. The coding sequence expands

over 650 amino acids, including a putative signal sequence starting at nucleotide 3653 with ATG. The unique *Nhe*I site cuts the DNA at position 988 of the given coding sequence within the coding part of amino acid 330, thereby separating the α -agglutinin into an N-terminal and a C-terminal part of about same size.

[0030] Through digestion of pUR2968 (see Figure 2) with *Nhe*I/*Hind*III a 1.4 kb fragment was released, containing the sequence information of the putative cell wall anchor. For the fusion to α -galactosidase the plasmid pSY16 was used, an episomal vector based on YEplac 181, harbouring the α -galactosidase sequence preceded by the *SUC2* invertase signal sequence and placed between the constitutive *PGK* promoter and *PGK* terminator. The *Sty*I site, present in the last nine base-pairs of the open reading frame of the α -galactosidase gene, was ligated to the *Nhe*I site of the *AGα1* gene fragment. To ensure the in frame fusion, the *Sty*I site was filled in and the 5' overhang of the *Nhe*I site was removed, prior to ligation into the *Sty*I/*Hind*III digested pSY13 (see Figure 2).

[0031] To verify the correct assembly of the new plasmid, the shuttle vector was transformed into *E. coli* JM109 (*recA1 supE44 endA1 hsdR17 gyrA96 relA1 thi* Δ (*lac-proAB*) F' [*traD36 proAB^r lacZ Δ M15*]) (see reference 7) by the transformation protocol described by Chung *et al.* (see reference 8). One of the positive clones, designated pUR2969, was further characterized, the DNA isolated and purified according to the Quiagen protocol and subsequently characterized by DNA sequencing. DNA sequencing was mainly performed as described by Sanger *et al.* (see reference 9), and Hsiao (see reference 10), here with the Sequenase version 2.0 kit from United States Biochemical Company, according to the protocol with T7 DNA polymerase (Amersham International plc) and [35 S]dATP α S (Amersham International plc: 370 MBq/ml; 22 TBq/mmol).

[0032] This plasmid was then transformed into *S. cerevisiae* strain MT302/1C according to the protocol from Klebe *et al.* (see reference 11).

[0033] Yeast transformants were selected on selective plates, lacking leucine, on with 40 μ l (20mg/ml DMF). X- α -Gal (5-bromo-4-chloro-3-indolyl- α -D-glucose, Boehringer Mannheim) was spread, to directly test for α -galactosidase activity (see reference 12). To demonstrate the expression, secretion, localization and activity of the chimeric protein the following analyses were performed:

1. Expression and secretion

[0034] *S. cerevisiae* strain MT302/1C was transformed with either plasmid pSY13 containing the α -galactosidase gene of *Cyamopsis tetragonoloba* or plasmid pUR2969 containing the α -galactosidase/ α -agglutinin fusion construct. During batch culture α -galactosidase activities were determined for washed cells and growth medium. The results are given in Figure 3 and Figure 4. The α -galactosidase expressed from yeast cells containing plasmid pSY13 was almost exclusively present in the growth medium (Figure 3A), whereas the α -galactosidase- α -agglutinin fusion protein was almost exclusively cell associated (Figure 4A). Moreover, the immobilized, cell wall-associated, α -galactosidase- α -agglutinin fusion enzyme had retained the complete activity over the whole incubation time, while the secreted and released enzyme lost about 90% of the activity after an incubation of 65 hours. This indicates, that the immobilization of the described enzyme into the cell wall of yeast protects the enzyme against inactivation, presumably through proteinases, and thereby increases the stability significantly. Further insight into the localization of the different gene products was obtained by Western analysis. Therefore, cells were harvested by centrifugation and washed in 10 mM Tris. HCl, pH 7.8; 1 mM PMSF at 0°C and all subsequent steps were performed at the same temperature. Three ml isolation buffer and 10 g of glass beads were added per gram of cells (wet weight). The mixture was shaken in a Griffin shaker at 50% of its maximum speed for 30 minutes. The supernatant was isolated and the glass beads were washed with 1 M NaCl and 1 mM PMSF until the washes were clear. The supernatant and the washes were pooled. The cell walls were recovered by centrifugation and were subsequently washed in 1 mM PMSF.

[0035] Non-covalently bound proteins or proteins bound through disulphide bridges were released from cell walls by boiling for 5 minutes in 50 mM Tris.HCl, pH 7.8; containing 2 % SDS, 100 mM EDTA and 40 mM β -mercaptoethanol. The SDS-extracted cell walls were washed several times in 1 mM PMSF to remove SDS. Ten mg of cell walls (wet weight) were taken up in 20 1 100 mM sodium acetate, pH 5.0, containing 1 mM PMSF. To this, 0.5 mU of the β -1,3-glucanase (Laminarase; Sigma L5144) was used as a source of β -1,3-glucanase) was added followed by incubation for 2 hours at 37 °C. Subsequently another 0.5 mU of β -1,3-glucanase was added, followed by incubation for another 2 hours at 37 °C.

[0036] Proteins were denatured by boiling for 5 minutes preceding Endo-H treatment. Two mg of protein were incubated in 1 ml 50 mM potassium phosphate, pH 5.5, containing 100 mM β -mercaptoethanol and 0.5 mM PMSF with 40 mU Endo-H (Boehringer) for 48 hours at 37 °C. Subsequently 20 mU Endo-H were added followed by 24 hours of incubation at 37 °C.

[0037] Proteins were separated by SDS-PAGE according to Laemmli (see reference 13) in 2.2.-20% gradient gels. The gels were blotted by electrophoretic transfer onto Immobilon polyvinylidene-difluoride membrane (Millipore) as described by Towbin *et al.* (see reference 14). In case of highly glycosylated proteins a subsequently mild periodate treatment was performed in 50 mM periodic acid, 100 mM sodium acetate, pH 4.5, for several hours at 4 °C. All

subsequent incubations were carried out at room temperature. The blot was blocked in PBS, containing 0.5% gelatine and 0.5% Tween-20, for one hour followed by incubation for 1 hour in probe buffer (PBS, 0.2% gelatine, 0.1% Tween-20) containing 1:200 diluted serum. The blot was subsequently washed several times in washing buffer (PBS; 0.2% gelatine; 0.5% Tween-20) followed by incubation for 1 hour in probe-buffer containing ^{125}I -labelled protein A (Amersham). After several washes in washing buffer, the blot was air-dried, wrapped in Saran (Dow) and exposed to X-omat S film (Kodak) with intensifying screen at -70 °C. An Omnimedia 6cx scanner and the Adobe Photoshop programme were used to quantify the amount of labelled protein. The results of the various protein isolation procedures from both transformants are given in Figure 5. While for the transformants comprising the pSY13 plasmid the overall mass of the enzyme was localized in the medium, with only minor amounts of enzyme more entrapped than bound in the cell wall (Figure 5A) -which could completely be removed by SDS extraction- the fusion protein was tightly bound to the cell wall; with only small amounts of α -galactosidase/ α -agglutinin delivered into the surrounding culture fluid or being SDS extractable. In contrast to the laminarinase extraction of cell walls from cells expressing the free α -galactosidase, where no further liberation of any more enzyme was observed, identical treatment of fusion enzyme expressing cells released the overall bulk of the enzyme. This indicates that the fusion protein is intimately associated with the cell wall glucan in *S. cerevisiae*, like α -agglutinin, while α -galactosidase alone is not. The subsequently performed EndoH treatment showed a heavy glycosylation of the fusion protein, a result, entirely in agreement with the described extended glycosylation of the C-terminal part of α -agglutinin.

2. Localization

[0038] Immunofluorescent labelling with anti- α -galactosidase serum was performed on intact cells to determine the presence and distribution of α -galactosidase/ α -agglutinin fusion protein in the cell wall. Immunofluorescent labelling was carried out without fixing according to Watzele *et al.* (see reference 15). Cells of $\text{OD}_{530}=2$ were isolated and washed in TBS (10 mM Tris.HCl, pH 7.8, containing 140 mM NaCl, 5 mM EDTA and 20 $\mu\text{g}/\text{ml}$ cycloheximide). The cells were incubated in TBS + anti- α -galactosidase serum for 1 hour, followed by several washings in TBS. A subsequent incubation was carried out with FITC-conjugated anti-rabbit IgG (Sigma) for 30 minutes. After washing in TBS, cells were taken up in 10 mM Tris.HCl, pH 9.0, containing 1 mg/ml p-phenylenediamine and 0.1 % azide and were photographed on a Zeiss 68000 microscope. The results of these analysis are given in Figure 6, showing clearly that the chimeric α -galactosidase/ α -agglutinin is localized at the surface of the yeast cell. Buds of various sizes, even very small ones very uniformly labelled, demonstrates that the fusion enzyme is continuously incorporated into the cell wall throughout the cell cycle and that it instantly becomes tightly linked.

3. Activity

[0039] To quantitatively assay α -galactosidase activity, 200 μl samples containing 0.1 M sodium-acetate, pH 4.5 and 10 mM p-nitrophenyl- α -D-galactopyranoside (Sigma) were incubated at 37 °C for exactly 5 minutes. The reaction was stopped by addition of 1 ml 2% sodium carbonate. From intact cells and cell walls, removed by centrifugation and isolated and washed as described, the α -galactosidase activity was calculated using the extinction coefficient of p-nitrophenol of 18.4 cm²/mole at 410 nm. One unit was defined as the hydrolysis of 1 μmole substrate per minute at 37 °C.

Table 1.

Distribution of free and immobilized α -galactosidase activity in yeast cells			
	α -Galactosidase activity (U/g F.W. cells)		
Expressed protein	Growth medium	Intact cells	Isolated cell walls
α -galactosidase	14.7	0.37	0.01
α Gal/ α AGG fusion protein	0.54	13.3	10.9

Transformed MT302/1C cells were in exponential phase ($\text{OD}_{530}=2$). One unit is defined as the hydrolysis of 1 μmole of p-nitrophenyl- α -D-galactopyranoside per minute at 37 °C.

[0040] The results are summarized in Table 1. While the overall majority of α -galactosidase was distributed in the culture fluid, most of the fusion product was associated with the cells, primarily with the cell wall. Taking together the results shown in Figures 3 to 6 and in Table 1, it could be calculated that the enzymatic α -galactosidase activity of the chimeric enzyme is as good as that of the free enzyme. Moreover, during stationary phase, the activity of the α -galactosidase in the growth medium decreased, whereas the activity of the cell wall associated α -galactosidase α -agglutinin fusion remained constant, indicating that the cell associated fusion protein is protected from inactivation or proteolytic

degradation.

[0041] N.B. The essence of this EXAMPLE was published during the priority year by M.P. Schreuder *et al.* (see reference 25).

5 EXAMPLE 2A Immobilized *Humicola lipase*/ α -agglutinin on the surface of *S. cerevisiae*. (inducible expression of immobilized enzyme system)

[0042] The construction and isolation of the 1.4 kb *NheI/HindIII* fragment containing the C-terminal part of α -agglutinin has been described in EXAMPLE 1. Plasmid pUR7021 contains an 894 bp long synthetically produced DNA fragment encoding the lipase of *Humicola* (see reference 16 and SEQ ID NO: 7 and 8), cloned into the *EcoRI/HindIII* restriction sites of the commercially available vector pTZ18R (see Figure 7). For the proper one-step modification of both the 5' end and the 3' end of the DNA part coding for the mature lipase, the PCR technique can be applied. Therefore the DNA oligonucleotides lipo1 (see SEQ ID NO: 3) and lipo2 (see SEQ ID NO: 6) can be used as primers in a standard PCR protocol, generating an 826 bp long DNA fragment with an *EagI* and a *HindIII* restriction site at the ends, which can be combined with the larger part of the *EagI/HindIII* digested pUR2650, a plasmid containing the α -galactosidase gene preceded by the invertase signal sequence as described earlier in this specification, thereby generating plasmid pUR2970A (see Figure 7).

[0043] PCR oligonucleotides for the in-frame linkage of *Humicola* lipase and the C-terminus of α agglutinin.

a: PCR oligonucleotides for the transition between *SUC2* signal sequence and the N-terminus of lipase.

25 primer lipol: >mature lipase
 EagI E V S Q D L P
 5'-GGG GCG GCC GAG GTC TCG CAA GAT CTG GA-3'
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
 lipase: 3'-TAA GCA GCT CTC CAG AGC GTT CTG GAC CTG TTT-5'
 (non-coding strand, see SEQ ID NO: 4)

b: PCR oligonucleotides for the in frame transition between C-terminus of lipase and C-terminal part of α -agglutinin.

F G L I G T C L
 lipase: 5'-TTC GGG TTA ATT GGG ACA TGT CTT TAG TGC GA-3'
 (cod. strand)
 primer 3'-CCC AAT TAA CCC TGT ACA GAA CGA TCG GAA TTC GAACCCC-5'
 lipo2:
 (for the part of the lipase coding strand see SEQ ID NO: 5)

[0044] Through the PCR method a *Nhe*I site will be created at the end of the coding sequence of the lipase, allowing the in-frame linkage between the DNA coding for lipase and the DNA coding for the C-terminal part of α -agglutinin. Plasmid pUR2970A can then be digested with *Nhe*I and *Hind*III and the 1.4 kb *Nhe*I/*Hind*III fragment containing the C-terminal part of α -agglutinin from plasmid pUR2968 can be combined with the larger part of *Nhe*I and *Hind*III treated plasmid pUR2970A, resulting in plasmid pUR2971A. From this plasmid the 2.2 kb *Eag*I/*Hind*III fragment can be isolated and ligated into the *Eag*I- and *Hind*III-treated pUR2741, whereby plasmid pUR2741 is a derivative of pUR2740 (see reference 17), where the second *Eag*I restriction site in the already inactive *Tet* resistance gene was deleted through *Nru*I/*Sal*I digestion. The *Sal*I site was filled in prior to religation. The ligation then results in pUR2972A containing the *GAL7* promoter, the invertase signal sequence, the chimeric lipase/ α -agglutinin gene, the 2 μ m sequence, the defective *Leu2* promoter and the *Leu2* gene. This plasmid can be used for transforming *S. cerevisiae* and the transformed cells can be cultivated in YP medium containing galactose as an inducer without repressing amounts of glucose being present, which causes the expression of the chimeric lipase/ α -agglutinin gene.

[0045] The expression, secretion, localization and activity of the chimeric lipase/ α -agglutinin can be analyzed using similar procedures as given in EXAMPLE 1.

[0046] In a similar way variants of *Humicola* lipase, obtained via rDNA techniques, can be linked to the C-terminal part of α -agglutinin, which variants can have a higher stability during (inter)esterification processes.

EXAMPLE 2B Immobilized *Humicola* lipase/α-agglutinin on the surface of *S. cerevisiae* (inducible expression of immobilized enzyme system)

[0047] EXAMPLE 2A describes a protocol for preparing a particular construct. Before carrying out the work it was considered more convenient to use the expression vector described in EXAMPLE 1, so that the construction route given in this EXAMPLE 2B differs on minor points from the construction route given in EXAMPLE 2A and the resulting plasmids are not identical to those described in EXAMPLE 2A. However, the essential gene construct comprising the promoter, signal sequence, and the structural gene encoding the fusion protein are the same in EXAMPLES 2A and 2B.

10 1. Construction

[0048] The construction and isolation of the 1.4 kb *Nhel/HindIII* fragment encoding the C-terminal part of α-agglutinin cell wall protein has been described in EXAMPLE 1. The plasmid pUR7033 (resembling pUR7021 of EXAMPLE 2A) was made by treating the commercially available vector pTZ18R with *EcoRI* and *HindIII* and ligating the resulting vector

15 fragment with an 894 bp long synthetically produced

[0049] DNA *EcoRI/HindIII* fragment encoding the lipase of *Humicola* (see SEQ ID NO: 7 and 8, and reference 16).

[0050] For the fusion of the lipase to the C-terminal, cell wall anchor-comprising domain of α-agglutinin, plasmid pUR7033 was digested with *EagI* and *HindIII*, and the lipase coding sequence was isolated and ligated into the *EagI*- and *HindIII*-digested yeast expression vector pSY1 (see reference 27), thereby generating pUR7034 (see Figure 13).

20 This is a 2μ episomal expression vector, containing the α-galactosidase gene described in EXAMPLE 1, preceded by the invertase (*SUC2*) signal sequence under the control of the inducible *GAL7* promoter.

[0051] Parallel to this digestion, pUR7033 was also digested with *EcoRV* and *HindIII*, thereby releasing a 57 bp long DNA fragment, possessing codons for the last 15 carboxyterminal amino acids. This fragment was exchanged against a small DNA fragment, generated through the hybridisation of the two chemically synthesized deoxyoligonucleotides

25 SEQ ID NO: 9 and SEQ ID NO: 10. After annealing of both DNA strands, these two oligonucleotides essentially reconstruct the rest of the 3' coding sequence of the initial lipase gene, but additionally introduce downstream of the lipase gene a new *Nhel* restriction site, followed by a *HindIII* site in close vicinity, whereby the first three nucleotides of the *Nhel* site form the codon for the last amino acid of the lipase. The resulting plasmid was designated pUR2970B. Subsequently, this construction intermediate was digested with *EagI* and *Nhel*, the lipase encoding fragment was

30 isolated, and, together with the 1.4 kb *Nhel/HindIII* fragment of pUR2968 ligated into the *EagI*- and *HindIII*-cut pSY1 vector. The outcome of this 3-point-ligation was called pUR2972B (see Figure 14), the final lipolase-α-agglutinin yeast expression vector.

[0052] This plasmid was used for transforming *S. cerevisiae* strain SU10 as described in reference 17 and the transformed cells were cultivated in YP medium containing galactose as the inducer without repressing amounts of glucose being present, which causes the expression of the chimeric lipase/α-agglutinin gene.

2. Activity

[0053] To quantify the lipase activity, two activity measurements with two separate substrates were performed. In both cases, SU10 yeast cells transformed with either plasmid pUR7034 or pSY1 served as control. Therefore, yeast cell transformants containing either plasmid pSY1 or plasmid pUR7034 or plasmid pUR2972B were grown up for 24h

40 in YNB-glucose medium supplied with histidine and uracil, then diluted 1:10 in YP-medium supplied with 5% galactose, and again cultured. After 24h incubation at 30°C, a first measurement for both assays was performed.

[0054] The first assay applied was the pH stat method. Within this assay, one unit of lipase activity is defined as the amount of enzyme capable of liberating one micromole of fatty acid per minute from a triglyceride substrate under standard assay conditions (30 ml assay solution containing 38 mM olive oil, considered as pure trioleate, emulsified with 1:1 w/w gum arabic, 20 mM calcium chloride, 40 mM sodium chloride, 5 mM Tris, pH 9.0, 30°C) in a radiometer pH stat apparatus (pHM 84 pH meter, ABU 80 autoburette, TTA 60 titration assembly). The fatty acids formed were titrated with 0.05 N NaOH and the activity measured was based on alkali consumption in the interval between 1 and 2 minutes after addition of putative enzyme batch. To test for immobilized lipase activity, 1 ml of each culture was centrifuged, the supernatant was saved, the pellet was resuspended and washed in 1 ml 1 M sorbitol, subsequently again centrifuged and resuspended in 200μl 1 M sorbitol. From each type of yeast cell the first supernatant and the washed cells were tested for lipase activity.

A: Lipase activity after 24h (LU/ml)		
	cell bound	culture fluid
pSY1	5.9	8.8
pUR7034	24.1	632.0
pUR2972B-(1)	18.7	59.6
pUR2972B-(2)	24.6	40.5

5

B: Lipase activity after 48h (LU/ml)			
	cell bound	culture fluid	OD660
pSY1	6.4	4.3	-40
pUR7034	215.0	2750.0	-40
pUR2972B-(1)	37.0	87.0	-40
pUR2972B-(2)	34.0	82.0	-40

10

- [0055] The rest of the yeast cultures was further incubated, and essentially the same separation procedure was done after 48 hours. Dependent on the initial activity measured, the actual volume of the sample measured deviated between 25µl and 150µl.
- [0056] This series of measurements indicates, that yeast cells comprising the plasmid coding for the lipase-α-agglutinin fusion protein in fact express some lipase activity which is associated with the yeast cell.

[0057] An additional second assay was performed to further confirm the immobilization of activity of lipase on the yeast cell surface. Briefly, within this assay, the kinetics of the PNP (=paranitrophenyl) release from PNP-butyrate is determined by measurement of the OD at 400 nm. Therefore, 10 ml cultures containing yeast cells with either pSY1, pUR7034 or pUR2972B were centrifuged, the pellet was resuspended in 4 ml of buffer A (0.1 M NaOAc, pH 5.0 and 1 mM PMSF), from this 4 ml 500µl was centrifuged again and resuspended in 500 µl PNB-buffer (20 mM Tris-HCl, pH 9.0, 20 mM CaCl₂, 25 mM NaCl), centrifuged once again, and finally resuspended in 400µl PNB buffer. This fraction was used to determine the cell bound fraction of lipase.

[0058] The remaining 3500µl were spun down, the pellet was resuspended in 4 ml A, to each of this, 40µl laminarinase (ex mollusc, 1.25 mU/µl) was added and first incubated for 3 hours at 37°C, followed by an overnight incubation at 20°C. Then the reaction mixture, still containing intact cells, were centrifuged again and the supernatant was used to determine the amount of originally cell wall bound material released through laminarinase incubation. The final pellet was resuspended in 400µl PNP buffer, to calculate the still cell associated part. The blank reaction of a defined volume of specific culture fraction in 4 ml assay buffer was determined, and than the reaction was started through addition of 80µl of substrate solution (100 mM PNP-butyrate in methanol), and the reaction was observed at 25°C at 400 nm in a spectrophotometer.

40

	cell bound activity*	activity in the medium	laminarinase extract	laminarinase extracted cells	OD660
pSY1	0.001 (116µl)	0.001	0.028	0.000	2.6
pUR7034	0.293 (220µl)	0.446	0.076	0.985	2.36
pUR2972B-(1)	0.494 (143µl)	0.021	0.170	0.208	2.10

45

* unless otherwise mentioned, the volume of enzyme solution added was 20µl

[0059] This result positively demonstrates that a significant amount of lipase activity is immobilized on the surface yeast cell, containing plasmid pUR2972B. Here again, incorporation took place in such a way, that the reaction was catalyzed by cell wall inserted lipase of intact cells, indicated into the exterior orientated immobilization. Furthermore, the release of a significant amount of lipase activity after incubation with laminarinase again demonstrates the presumably covalent incorporation of a heterologous enzyme through gene fusion with the C-terminal part of α-agglutinin.

55

3. Localization

[0060] The expression, secretion, and subsequent incorporation of the lipase-α-agglutinin fusion protein into the

yeast cell wall was also confirmed through immunofluorescent labelling with anti-lipolase serum essentially as described in EXAMPLE 1, item 2. Localization.

[0061] As can be seen in Figure 15, the immunofluorescent stain shows essentially an analogous picture as the α -galactosidase immuno stain, with clearly detectable reactivity on the outside of the cell surface (see Figure 15 A showing a clear halo around the cells and Figure B showing a lighter circle at the surface of the cells), but neither in the medium nor in the interior of the cells. Yeast cells expressing pUR2972B, the *Humicola* lipase- α -agglutinin fusion protein, become homogeneously stained on the surface, indicating the virtually entire immobilization of a chimeric enzyme with an α -agglutinin C-terminus on the exterior of a yeast cell. In the performed control experiment SU10 yeast cells containing plasmid pUR7034 served as a control and here, no cell surface bound reactivity against the applied anti-lipase serum could be detected.

[0062] In a similar way variants of *Humicola* lipase, obtained via rDNA techniques, can be linked to the C-terminal part of α -agglutinin, which variants can have a higher stability during (inter)esterification processes.

EXAMPLE 3 Immobilized *Humicola* lipase/ α -agglutinin on the surface of *S. cerevisiae* (constitutive expression of immobilized enzyme system)

[0063] Plasmid pUR2972 as described in EXAMPLE 2 can be treated with *EagI* and *HindIII* and the about 2.2 kb fragment containing the lipase/ α -agglutinin gene can be isolated. Plasmid pSY16 can be restricted with *EagI* and *HindIII* and between these sites the 2.2 kb fragment containing the lipase/ α -agglutinin fragment can be ligated resulting in pUR2973. The part of this plasmid that is involved in the production of the chimeric enzyme is similar to pUR2972 with the exception of the signal sequence. Whereas pUR2972 contains the SUC2-invertase-signal sequence, pUR2973 contains the α -mating factor signal sequence (see reference 18). Moreover the plasmid pUR2973 contains the *Leu2* marker gene with the complete promoter sequence, instead of the truncated promoter version of pUR2972.

EXAMPLE 4 Immobilized *Geotrichum* lipase/ α -agglutinin on the surface of *S. cerevisiae*

[0064] The construction and isolation of the 1.4 kb *NheI/HindIII* fragment comprising the C-terminal part of AG α -1 (α -agglutinin) gene has been described in EXAMPLE 1. For the in-frame gene fusion of the DNA coding for the C-terminal membrane anchor of α -agglutinin to the complete coding sequence of *Geotrichum candidum* lipase B from strain CMICC 335426 (see Figure 8 and SEQ ID NO: 11 and 12), the plasmid pUR2974 can be used. This plasmid, derived from the commercially available pBluescript II SK plasmid, contains the cDNA coding for the complete *G. candidum* lipase II on an 1850 bp long *EcoRI/Xhol* insert (see Figure 9).

[0065] To develop an expression vector for *S. cerevisiae* with homologous signal sequences, the N-terminus of the mature lipase B was determined experimentally by standard techniques. The obtained amino acid sequence of "Gln-Ala-Pro-Thr-Ala-Val..." is in complete agreement with the cleavage site of the signal peptidase on the *G. candidum* lipase II (see reference 19).

[0066] For the fusion of the mature lipase B to the *S. cerevisiae* signal sequences of SUC2 (invertase) or α -mating factor (prepro- α MF) on one hand and the in-frame fusion to the 3' part of the AG α -1 gene PCR technique can be used. The PCR primer lipo3 (see SEQ ID NO: 13) can be constructed in such a way, that the originally present *EagI* site in the 5'-part of the coding sequence (spanning codons 5-7 of the mature protein) will become inactivated without any alteration in the amino acid sequence.

[0067] To facilitate the subsequent cloning procedures, the PCR primer can further contain a new *EagI* site at the 5' end, for the in-frame ligation to SUC2 signal sequence or prepro- α MF sequence, respectively. The corresponding PCR primer lipo4 (see SEQ ID NO: 16) contains an extra *NheI* site behind the nucleotides coding for the C-terminus of lipase B, to ensure the proper fusion to the C-terminal part of α -agglutinin.

PCR oligonucleotides for the in frame linkage of *G. candidum* lipase II to the SUC2 signal sequence and the C-terminal part of α -agglutinin.

a: N-terminal transition to either prepro α MF sequence or SUC2 signal sequence.

50
EagI A Q A P R P S L N
 primer lipo3: 5'-GGG GCG GCC GCG CAG GCC CCA AGG CGG TCT CTC AAT-3'
 55
 lipaseII: 3'-GAC CGG GTC CGG GGT GCC GCC AGA GAG TTA-5'
 (non-cod. strand, see SEQ ID NO: 14))

b: C-terminal fusion to C part of α -agglutinin

S N F E T D V N L Y G
 lipase: 5'-CA AAC TTT GAG ACT GAC GTT AAT CTC TAC GGT TAA AAC-3'
 (cod. strand)
 primer lipo4: 3'-C TGA CTG CAA TTA GAG ATG CCA CGATCG CCCC-5'
 (for the part of the lipase coding strand see SEQ ID NO: 15)
NheI

- [0068] The PCR product with the modified ends can be generated by standard PCR protocols, using instead of the normal Ampli-Taq polymerase the new thermostable VENT polymerase, which also exhibits proofreading activity, to ensure an error-free DNA template. Through digestion of the formerly described plasmid pUR2972 with *Eag*I (complete) and *Nhe*I (partial), the *Humicola* lipase fragment can be exchanged against the DNA fragment coding for lipase B, thereby generating the final *S. cerevisiae* expression vector pUR2975 (see Figure 9).

- [0069] The *Humicola* lipase- α -agglutinin fusion protein coding sequence can be exchanged against the lipase B/ α -agglutinin fusion construct described above by digestion of the described vector pUR2973 with *EagI/HindIII*, resulting in pUR2976 (see Figure 9).

EXAMPLE 5 Immobilized *Rhizomucor miehei* lipase/α-agglutinin on the surface of *S. cerevisiae*

- [0070] The construction and isolation of the 1.4 kb *NheI/HindIII* fragment encoding the C-terminal part of α -agglutinin has been described in EXAMPLE 1. The plasmid pUR2980 contains a 1.25 kb cDNA fragment cloned into the *SmaI* site of commercially available pUC18, which (synthetically synthesizable) fragment encodes the complete coding sequence of triglyceride lipase of *Rhizomucor miehei* (see reference 20), an enzyme used in a number of processes to interesterify triacylglycerols (see reference 21) or to prepare biosurfactants (see reference 22). Beside the 269 codons of the mature lipase molecule, the fragment also harbours codons for the 24 amino acid signal peptide as well as 70 amino acids of the propeptide. PCR can easily be applied to ensure the proper fusion of the gene fragment encoding the mature lipase to the *SUC2* signal sequence or the prepro α -mating factor sequence of *S. cerevisiae*, as well as the in-frame fusion to the described *NheI/HindIII* fragment. The following two primers, lipo5 (see SEQ ID NO: 17) and lipo6 (see SEQ ID NO: 20), will generate a 833 bp DNA fragment, which after Proteinase K treatment and digestion with *EagI* and *NheI* can be cloned as an 816 bp long fragment into the *EagI/NheI* digested plasmids pUR2972 and pUR2973, respectively (see Figure 7).

EagI A S I D G G I
lipo5: 5'-CCC GCG GCC GCG AGC ATT GAT GGT GGT ATC-3'.
lipase (non-cod. strand): 3'-TCG TAA CTA GCA CCA TAG-5'.
(for the part of the lipase non-coding strand see SEQ ID NO: 18)

lipase (cod. strand): 5'-AAC ACA GGC CTC TGT ACT-3'
Lipo6: 3'-TTG TGT CCG GAG ACA TGA CGATCGCGCC-5'
NheI
(for the part of the lipase coding strand see SEQ ID NO: 19)

- [0071] These new *S. cerevisiae* expression plasmids contain the *GAL7* promoter, the invertase signal sequence (pUR2981) or the prepro- α -mating factor sequence (pUR2982), the chimeric *Rhizomucor miehei* lipase/ α -agglutinin gene, the 2 μ m sequence, the defective (truncated) *Leu2* promoter and the *Leu2* gene. These plasmids can be transformed into *S. cerevisiae* and grown and analyzed using protocols described in earlier EXAMPLES.

EXAMPLE 6 Immobilized *Aspergillus niger* glucose oxidase/GPI anchored cell wall proteins on the surface of *S. cerevisiae*

- [0072] Glucose oxidase (β -D:oxygen 1-oxidoreductase, EC 1.1.3.4) from *Aspergillus niger* catalyses the oxidation of β -D-glucose to glucono- δ -lactone and the concomitant reduction of molecular oxygen to hydrogen peroxide. The fungal enzyme consists of a homodimer of molecular weight 150,000 containing two tightly bound FAD co-factors. Beside the use in glucose detection kits the enzyme is useful as a source of hydrogen peroxide in food preservation.

The gene was cloned from both cDNA and genomic libraries, the single open reading frame contains no intervening sequences and encodes a protein of 605 amino acids (see reference 23).

[0073] With the help of two proper oligonucleotides the coding part of the sequence is adjusted in a one-step modifying procedure by PCR in such a way that a fusion gene product will be obtained coding for glucose oxidase and the C-terminal cell wall anchor of the *FLO1* gene product or α -agglutinin. Thus, some of the plasmids described in former EXAMPLES can be utilized to integrate the corresponding sequence in-frame between one of the signal sequences used in the EXAMPLES and the *NheI/HindIII* part of the *AGA1* gene.

[0074] Since dimerisation of the two monomers might be a prerequisite for activity, in an alternative approach the complete coding sequence for glucose oxidase without the GPI anchor can be expressed in *S. cerevisiae* transformant which already contains the fusion construct. This can be fulfilled by constitutive expression of the fusion construct containing the GPI anchor with the help of the *GAPDH* or *PGK* promoter for example. The unbound not-anchored monomer can be produced by using a DNA construct comprising an inducible promoter, as for instance the *GAL7* promoter.

EXAMPLE 7 Process to convert raffinose, stachyose and similar sugars in soy extracts with α -galactosidase/ α -agglutinin immobilized on yeasts

[0075] The yeast transformed with plasmid pUR2969 can be cultivated on large scale. At regular intervals during cultivation the washed cells should be analyzed on the presence of α -galactosidase activity on their surface with methods described in EXAMPLE 1. When both cell density and α -galactosidase activity/biomass reach their maximum, the yeast cells can then be collected by centrifugation and washed. The washed cells can then be added to soy extracts. The final concentration of the yeast cells can vary between 0.1 and 10 g/l, preferably the concentration should be above 1 g/l. The temperature of the soy extract should be < 8 °C to reduce the metabolic activity of the yeast cells. The conversion of raffinose and stachyose can be analyzed with HPLC methods and after 95 % conversion of these sugars the yeasts cells can be removed by centrifugation and their α -galactosidase activity/g biomass can be measured. Centrifugates with a good activity can be used in a subsequent conversion process, whereas centrifugates with an activity of less than 50 % of the original activity can be resuscitated in the growth medium and the cells can be allowed to recover for 2 to 4 hours. Thereafter the cells can be centrifuged, washed and subsequently be used in a subsequent conversion process.

EXAMPLE 8 Production of biosurfactants using *Humicola* lipase/ α -agglutinin immobilized on yeasts.

[0076] The yeast transformed with plasmid pUR2972 or pUR2973 can be cultivated on large scale. At regular intervals during cultivation the washed cells can be analyzed on the presence of lipase activity on their surface with methods described in EXAMPLE 1. When both cell density and lipase/biomass reache their maximum, the yeast cells can be collected by centrifugation and washed. The washed cells can be suspended in a small amount of water and added to a reactor tank containing a mix of fatty acids, preferably of a chain length between 12-18 carbon atoms and sugars, preferably glucose, galactose or sucrose. The total concentration of the water (excluding the water in the yeast cells) might be below 0.1 %. The final concentration of the yeast cells can vary between 0.1 and 10 g/l, preferably the concentration is above 1 g/l. The tank has to be kept under an atmosphere of N₂ and CO₂ in order to avoid oxidation of the (unsaturated) fatty acids and to minimize the metabolic activity of the yeasts. The temperature of mixture in the tank should be between 30-60 °C, depending on type of fatty acid used. The conversion of fatty acids can be analyzed with GLC methods and after 95 % conversion of these fatty acids the yeasts cells can be removed by centrifugation and their lipase activity/g biomass can be measured. Centrifugates with a good activity can be used in a subsequent conversion process, whereas centrifugates with an activity of less then 50 % of the original activity can be resuscitated in the growth medium and the cells can be allowed to recover for 2 to 8 hours. Thereafter the cells can be centrifuged again, washed and used in a subsequent conversion process.

EXAMPLE 9 Production of special types of triacylglycerols using *Rhizomucor miehei* lipase/ α -agglutinin immobilized on yeasts.

[0077] The yeast transformed with plasmid pUR2981 or pUR2982 can be cultivated on a large scale. At regular intervals during cultivation the washed cells can be analyzed on the presence of lipase activity on their surface with methods described in EXAMPLE 1. When both cell density and lipase/biomass reach their maximum, the yeast cells can be collected by centrifugation and washed. The washed cells can be suspended in a small amount of water and can be added to a reactor tank containing a mix of various triacylglycerols and fatty acids. The total concentration of the water (excluding the water in the yeast cells) might be below 0.1 %. The final concentration of the yeast cells can vary between 0.1 and 10 g/l, preferably the concentration is above 1 g/l. The tank has to be kept under an atmosphere

of N_2 and CO_2 in order to avoid oxidation of the (unsaturated) fatty acids and to minimize the metabolic activity of the yeasts. The temperature of mixture in the tank should be between 30-70 °C, depending on types of triacylglycerol and fatty acid used. The degree of interesterification can be analyzed with GLC/MS methods and after formation of at least 80 % of the theoretical value of the desired type of triacylglycerol the yeasts cells can be removed by centrifugation and their lipase activity/g biomass can be measured. Centrifugates with a good activity can be used in a subsequent conversion process, whereas centrifugates with an activity of less than 50 % of the original activity is resuscitated in the growth medium and the cells should be allowed to recover 2 to 8 hours. After that the cells can be centrifuged, washed and used in a subsequent interesterification process.

[0078] Baker's yeasts of strain MT302/1C, transformed with either plasmid pSY13 or plasmid pUR2969 (described in EXAMPLE 1) were deposited under the Budapest Treaty at the Centraalbureau voor Schimmelcultures (CBS) on 3 July 1992 under provisional numbers 330.92 and 329.92, respectively.

EXAMPLE 10 Immobilized *Humicola* lipase/FLO1 fusion on the surface of *S. cerevisiae*

[0079] Flocculation, defined as "the (reversible) aggregation of dispersed yeast cells into flocs" (see reference 24), is the most important feature of yeast strains in industrial fermentations. Beside this it is of principal interest, because it is a property associated with cell wall proteins and it is a quantitative characteristic. One of the genes associated with the flocculation phenotype in *S. cerevisiae* is the *FLO1* gene. The gene is located at approximately 24 kb from the right end of chromosome I and the DNA sequence of a clone containing major parts of *FLO1* gene has very recently been determined (see reference 26). The sequence is given in Figure 11 and SEQ ID NO: 21 and 22. The cloned fragment appeared to be approximately 2 kb shorter than the genomic copy as judged from Southern and Northern hybridizations, but encloses both ends of the *FLO1* gene. Analysis of the DNA sequence data indicates that the putative protein contains at the N-terminus a hydrophobic region which confirms a signal sequence for secretion, a hydrophobic C-terminus that might function as a signal for the attachment of a GPI-anchor and many glycosylation sites, especially in the C-terminus, with 46,6 % serine and threonine in the arbitrarily defined C-terminus (aa 271-894). Hence, it is likely that the *FLO1* gene product is localized in an orientated fashion in the yeast cell wall and may be directly involved in the process of interaction with neighbouring cells. The cloned *FLO1* sequence might therefore be suitable for the immobilization of proteins or peptides on the cell surface by a different type of cell wall anchor.

[0080] Recombinant DNA constructs can be obtained, for example by utilizing the DNA coding for amino acids 271-894 of the *FLO1* gene product, i.e. polynucleotide 811-2682 of Figure 11. Through application of two PCR primers pcrf1o1 (see SEQ ID NO: 23) and pcrf1o2 (see SEQ ID NO: 26) *NheI* and *HindIII* sites can be introduced at both ends of the DNA fragment. In a second step, the 1.4 kb *NheI/HindIII* fragment present in pUR2972 (either A or B) containing the C-terminal part of α -agglutinin can be replaced by the 1.9 kb DNA fragment coding for the C-terminal part of the *FLO1* protein, resulting in plasmid pUR2990 (see Figure 12), comprising a DNA sequence encoding (a) the invertase signal sequence (*SUC2*) preceding (b) the fusion protein consisting of (b.1) the lipase of *Humicola* (see reference 16) followed by (b.2) the C-terminus of *FLO1* protein (aa 271-894).

PCR oligonucleotides for the in frame connection of the genes encoding the *Humicola* lipase and the C-terminal part of the *FLO1* gene product.

40
 primer pcrf1o1 S N Y A V S T
 5' - CAATTG GCT AGC AAT TAT GCT GTC AGT ACC - 3'
NheI ||| ||| ||| ||| ||| |||
FLO1 gene (non-coding strand) 3' - AGT TTA ATA CGA CAG TCA TGG TGA - 5'
 (for the part of the non-coding strand see SEQ ID NO: 24)

45
 50
FLO1 coding strand 5'-ATAAA AATTGGCGTTCTTTTACG - 3'
 primer pcrf1o2: 3' - TTAAGCGCAAGAAAAATGC TTCGAACCTCGAG - 5'
HindIII
 (for the part of the coding strand see SEQ ID NO: 25)

[0081] Plasmid pUR2972 (either A or B) can be restricted with *NheI* (partial) and *HindIII* and the *NheI/HindIII* fragment comprising the vector backbone and the lipase gene can be ligated to the correspondingly digested PCR product of the plasmid containing the *FLO1* sequence, resulting in plasmid pUR2990, containing the *GAL7* promoter, the *S. cerevisiae* invertase signal sequence, the chimeric lipase/*FLO1* gene, the yeast 2 μ m sequence, the defective *Leu2* promoter and the *Leu2* gene. This plasmid can be transformed into *S. cerevisiae* and the transformed cells can be cultivated

in YP medium including galactose as inductor.

[0082] The expression, secretion, localization and activity of the chimeric lipase/FLO1 protein can be analyzed using similar procedures as given in Example 1.

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[0083]

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5 SEQUENCE LISTING

[0084]

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10

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(ii) TITLE OF INVENTION: Enzymic Processes based on naturally immobilized enzymes that can easily be separated and regenerated

50 (iii) NUMBER OF SEQUENCES: 26

(iv) COMPUTER READABLE FORM:

55

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6057 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Saccharomyces cerevisiae*

(ix) FEATURE:

- 20 (A) NAME/KEY: CDS
- (B) LOCATION: 3653..5605
- (D) OTHER INFORMATION: /function= "sexual agglutinisation" /product= "alpha-agglutinin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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	TTGTCTGATT TTAGTAGTAC CGGAAGGTTT ATTACGCCA AGAACAGTGC TTGAATTGAG	180
35	TTCTCGGGAC ACGGGAAAGA CAATGGAAGA AAAATTTACA TTCAGTAGCC TTATATATGA	240
	AATGCTGCCA AGCCACGTCT TTATAAGTAG ATAATGTCCC ATGAGCTGAA CTATGGGAAT	300
40	TTATGACGCA GTTCATTGTA TATATATTAC ATTAACTCTT TAGTTAACCA TCTGAATTGT	360
	TTTATAAAAT AACTTTTGTA ATTTTTTAT GATCGCTTAG TTAAGTCTAT TATATCAGGT	420
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40	GTAAGTGATA TCCATGAATG GGAATAGGCT TTGAACTTG ACGATTTAGT TCCTTATTTC	2880
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	AAGAAGACTA TACATATGCA TTATTCTTAA CCAAGACCCAC TATGAATAGT AATACCATAT	3060
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	5 10 15	
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	20 25 30	
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	Pro Leu Thr Ala Asn Lys Gln Pro Asp Gln Gly Trp Thr Ala Thr Phe	
	35 40 45	
35	GAT TTT AGT ATT GCA GAT GCG TCT TCC ATT AGG GAG GGC GAT GAA TTC	3847
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	Thr Leu Ser Met Pro His Val Tyr Arg Ile Lys Leu Leu Asn Ser Ser	
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25		
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	CAA TTT ACA TCC TCT TCT TTC GCA ACA ATC AAC AGC ACA CCA ATA ATC Gln Phe Thr Ser Ser Ser Phe Ala Thr Ile Asn Ser Thr Pro Ile Ile 450 455 460 465	5047
55		

	TCT TCA TCA GCA GTA TTT GAA ACC TCA GAT GCT TCA ATT GTC AAT GTG Ser Ser Ser Ala Val Phe Glu Thr Ser Asp Ala Ser Ile Val Asn Val 5	470	475	480	5095
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	GAA ACA GCA CTC TCA TCT CAG GGA ACG AAA ATT GAC ACC TTT TTA GTG Glu Thr Ala Leu Ser Ser Gln Gly Thr Lys Ile Asp Thr Phe Leu Val 40	580	585	590	5431
	TCA TCC TTG ATC GCA TAT CCT TCT GCA TCA GGA AGC CAA TTG TCC Ser Ser Leu Ile Ala Tyr Pro Ser Ser Ala Ser Gly Ser Gln Leu Ser 45	595	600	605	5479
	GCT ATC CAA CAG AAT TTC ACA TCA ACT TCT CTC ATG ATT TCA ACC TAT Gly Ile Gln Gln Asn Phe Thr Ser Thr Ser Leu Met Ile Ser Thr Tyr 50	610	615	620	5527
	GAA GGT AAA GCG TCT ATA TTT TTC TCA GCT GAG CTC GGT TCG ATC ATT Glu Gly Lys Ala Ser Ile Phe Phe Ser Ala Glu Leu Gly Ser Ile Ile 55	630	635	640	5575

TTT CTG CTT TTG TCG TAC CTG CTA TTC TAAAACGGGT ACTGTACAGT Phe Leu Leu Leu Ser Tyr Leu Leu Phe	5622
5 645 650	
 TAGTACATTG AGTCGAAATA TACGAAATTA TTGTTCATAA TTTTCATCCT GGCTCTTTT	5682
10 TTCTTCAACC ATAGTTAAAT GGACAGTTCA TATCTTAAAC TCTAATAATA CTTTTCTAGT	5742
 TCTTATCCTT TTCCGTCTCA CCGCAGATT TATCATAGTA TTAAATTAT ATTTTGTTCG	5802
15 TAAAAAGAAA AATTTGTGAG CGTTACCGCT CGTTTCATTA CCCGAAGGCT GTTTCAGTAG	5862
ACCACTGATT AACTAAGTAG ATGAAAAAAT TTCATCACCA TGAAAGAGTT CGATGAGAGC	5922
20 TACTTTTCA AATGCTTAAC AGCTAACCGC CATTCAATAA TGTTACGTTC TCTTCATTCT	5982
GCGGCTACGT TATCTAACAA GAGGTTTAC TCTCTCATAT CTCATTCAA TAGAAAGAAC	6042
25 ATAATCAAAA AGCTT	6057

(2) INFORMATION FOR SEQ ID NO: 2:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 650 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

40 Met Phe Thr Phe Leu Lys Ile Ile Leu Trp Leu Phe Ser Leu Ala Leu 1 5 10 15
45 Ala Ser Ala Ile Asn Ile Asn Asp Ile Thr Phe Ser Asn Leu Glu Ile 20 25 30
50 Thr Pro Leu Thr Ala Asn Lys Gln Pro Asp Gln Gly Trp Thr Ala Thr 35 40 45
55 Phe Asp Phe Ser Ile Ala Asp Ala Ser Ser Ile Arg Glu Gly Asp Glu 50 55 60

55

Phe Thr Leu Ser Met Pro His Val Tyr Arg Ile Lys Leu Leu Asn Ser
 65 70 75 80
 5 Ser Gln Thr Ala Thr Ile Ser Leu Ala Asp Gly Thr Glu Ala Phe Lys
 85 90 95
 10 Cys Tyr Val Ser Gln Gln Ala Ala Tyr Leu Tyr Glu Asn Thr Thr Phe
 100 105 110
 15 Thr Cys Thr Ala Gln Asn Asp Leu Ser Ser Tyr Asn Thr Ile Asp Gly
 115 120 125
 Ser Ile Thr Phe Ser Leu Asn Phe Ser Asp Gly Gly Ser Ser Tyr Glu
 130 135 140
 20 Tyr Glu Leu Glu Asn Ala Lys Phe Phe Lys Ser Gly Pro Met Leu Val
 145 150 155 160
 25 Lys Leu Gly Asn Gln Met Ser Asp Val Val Asn Phe Asp Pro Ala Ala
 165 170 175
 Phe Thr Glu Asn Val Phe His Ser Gly Arg Ser Thr Gly Tyr Gly Ser
 180 185 190
 30 Phe Glu Ser Tyr His Leu Gly Met Tyr Cys Pro Asn Gly Tyr Phe Leu
 195 200 205
 35 Gly Gly Thr Glu Lys Ile Asp Tyr Asp Ser Ser Asn Asn Asn Val Asp
 210 215 220
 40 Leu Asp Cys Ser Ser Val Gln Val Tyr Ser Ser Asn Asp Phe Asn Asp
 225 230 235 240
 45 Trp Trp Phe Pro Gln Ser Tyr Asn Asp Thr Asn Ala Asp Val Thr Cys
 245 250 255
 Phe Gly Ser Asn Leu Trp Ile Thr Leu Asp Glu Lys Leu Tyr Asp Gly
 260 265 270
 50 Glu Met Leu Trp Val Asn Ala Leu Gln Ser Leu Pro Ala Asn Val Asn
 275 280 285
 55 Thr Ile Asp His Ala Leu Glu Phe Gln Tyr Thr Cys Leu Asp Thr Ile
 290 295 300

Ala Asn Thr Thr Tyr Ala Thr Gln Phe Ser Thr Thr Arg Glu Phe Ile
 305 310 315 320

5 Val Tyr Gln Gly Arg Asn Leu Gly Thr Ala Ser Ala Lys Ser Ser Phe
 325 330 335

10 Ile Ser Thr Thr Thr Asp Leu Thr Ser Ile Asn Thr Ser Ala Tyr
 340 345 350

15 Ser Thr Gly Ser Ile Ser Thr Val Glu Thr Gly Asn Arg Thr Thr Ser
 355 360 365

Glu Val Ile Ser His Val Val Thr Thr Ser Thr Lys Leu Ser Pro Thr
 370 375 380

20 Ala Thr Thr Ser Leu Thr Ile Ala Gln Thr Ser Ile Tyr Ser Thr Asp
 385 390 395 400

25 Ser Asn Ile Thr Val Gly Thr Asp Ile His Thr Thr Ser Glu Val Ile
 405 410 415

Ser Asp Val Glu Thr Ile Ser Arg Glu Thr Ala Ser Thr Val Val Ala
 420 425 430

30 Ala Pro Thr Ser Thr Thr Gly Trp Thr Gly Ala Met Asn Thr Tyr Ile
 435 440 445

35 Pro Gln Phe Thr Ser Ser Ser Phe Ala Thr Ile Asn Ser Thr Pro Ile
 450 455 460

40 Ile Ser Ser Ser Ala Val Phe Glu Thr Ser Asp Ala Ser Ile Val Asn
 465 470 475 480

Val His Thr Glu Asn Ile Thr Asn Thr Ala Ala Val Pro Ser Glu Glu
 485 490 495

45 Pro Thr Phe Val Asn Ala Thr Arg Asn Ser Leu Asn Ser Phe Cys Ser
 500 505 510

50 Ser Lys Gln Pro Ser Ser Pro Ser Ser Tyr Thr Ser Ser Pro Leu Val
 515 520 525

55 Ser Ser Leu Ser Val Ser Lys Thr Leu Leu Ser Thr Ser Phe Thr Pro
 530 535 540

Ser Val Pro Thr Ser Asn Thr Tyr Ile Lys Thr Glu Asn Thr Gly Tyr
 545 550 555 560

5

Phe Glu His Thr Ala Leu Thr Thr Ser Ser Val Gly Leu Asn Ser Phe
 565 570 575

10 Ser Glu Thr Ala Leu Ser Ser Gln Gly Thr Lys Ile Asp Thr Phe Leu
 580 585 590

15 Val Ser Ser Leu Ile Ala Tyr Pro Ser Ser Ala Ser Gly Ser Gln Leu
 595 600 605

20 Ser Gly Ile Gln Gln Asn Phe Thr Ser Thr Ser Leu Met Ile Ser Thr
 610 615 620

Tyr Glu Gly Lys Ala Ser Ile Phe Phe Ser Ala Glu Leu Gly Ser Ile
 625 630 635 640

25 Ile Phe Leu Leu Ser Tyr Leu Leu Phe
 645 650

30

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 40 (ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: primer lipol

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGGCGGGCCG ACCTCTCGCA AGATCTGGA

29

50

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5 (vii) IMMEDIATE SOURCE:

(B) CLONE: Part non-coding strand lipase

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TTTGTCCAGG TCTTGCGAGA CCTCTCGACG AAT**33**

15 (2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (vii) IMMEDIATE SOURCE:

(B) CLONE: Part coding strand lipase

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTCGGGTTAA TTGGGACATG TCTTTAGTGC CA**32**

35

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

50 (B) CLONE: primer lipo2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

55 **CCCCAAGCTT AAGGCTAGCA AGACATGTCC CAATTAACCC****40**

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- 5
 (A) LENGTH: 894 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Humicola lanuginosa*

15 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 72..884
 (D) OTHER INFORMATION: /product= "lipase"

20 (ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 72..881
 (D) OTHER INFORMATION: /product= "lipase"

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

<code>GAATTCTGTAG CGACGATATG AGGAGCTCCC TTGTGCTGTT CTTTGTCTCT GCGTGGACGG</code> <code>CCTTGCCAC G GCC GAG GTC TCG CAA GAT CTG TTT AAC CAG TTC AAT CTC</code> <code>Ala Glu Val Ser Gln Asp Leu Phe Asn Gln Phe Asn Leu</code>	60 110
<code>1 5 10</code>	
<code>TTT GCA CAG TAT TCT GCT GCC GCA TAC TGC GGA AAA AAC AAT GAT GCC</code> <code>Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Gly Lys Asn Asn Asp Ala</code>	158
<code>15 20 25</code>	

40

45

50

55

	CCA GCT GGT ACA AAC ATT ACG TGC ACG GGA AAT GCC TGC CCC GAG GTA		206
5	Pro Ala Gly Thr Asn Ile Thr Cys Thr Gly Asn Ala Cys Pro Glu Val		
	30	35	40
			45
	GAG AAG GCG GAT GCA ACG TTT CTC TAC TCG TTT GAA GAC TCT GGA GTG		254
10	Glu Lys Ala Asp Ala Thr Phe Leu Tyr Ser Phe Glu Asp Ser Gly Val		
	50	55	60
15	GGC GAT GTC ACC GGC TTC CTT GCT CTA GAC AAC ACG AAC AAA TTG ATC		302
	Gly Asp Val Thr Gly Phe Leu Ala Leu Asp Asn Thr Asn Lys Leu Ile		
	65	70	75
20	GTC CTC TCT TTC CGT GGC TCT CGT TCC ATA GAA AAC TGG ATC GGA AAT		350
	Val Leu Ser Phe Arg Gly Ser Arg Ser Ile Glu Asn Trp Ile Gly Asn		
	80	85	90
25	CTT AAC TTC GAC TTG AAA GAA ATA AAT GAC ATT TGC TCC GGC TGC AGG		398
	Leu Asn Phe Asp Leu Lys Glu Ile Asn Asp Ile Cys Ser Gly Cys Arg		
	95	100	105
30	GGA CAT GAC GGC TTC ACC TCG AGC TGG AGG TCT GTA GCC GAT ACG TTA		446
	Gly His Asp Gly Phe Thr Ser Ser Trp Arg Ser Val Ala Asp Thr Leu		
	110	115	120
			125
35	AGG CAG AAG GTG GAG GAT GCT GTG AGG GAG CAT CCC GAC TAT CGC GTG		494
	Arg Gln Lys Val Glu Asp Ala Val Arg Glu His Pro Asp Tyr Arg Val		
	130	135	140
40	GTC TTT ACC GGA CAT AGC TTG GGT GCA TTG GCA ACT GTT GCC GGA		542
	Val Phe Thr Gly His Ser Leu Gly Gly Ala Leu Ala Thr Val Ala Gly		
	145	150	155
45	GCA GAC CTG CGT GGA AAT GGG TAT GAC ATC GAC GTG TTT TCA TAT GGC		590
	Ala Asp Leu Arg Gly Asn Gly Tyr Asp Ile Asp Val Phe Ser Tyr Gly		
	160	165	170
50	GCC CCC CGA GTC GGA AAC AGG GCT TTT GCA GAA TTC CTG ACC GTA CAG		638
	Ala Pro Arg Val Gly Asn Arg Ala Phe Ala Glu Phe Leu Thr Val Gln		
	175	180	185
55	ACC GGC GGT ACC CTC TAC CGC ATT ACC CAC ACC AAT GAT ATT GTC CCT		686
	Thr Gly Gly Thr Leu Tyr Arg Ile Thr His Thr Asn Asp Ile Val Pro		
	190	195	200
			205

AGA CTC CCG CCG CGC GAG TTC GGT TAC AGC CAT TCT AGC CCA GAG TAC Arg Leu Pro Pro Arg Glu Phe Gly Tyr Ser His Ser Ser Pro Glu Tyr	734	
210	215	220
5		
TGG ATC AAA TCT GGA ACC CTT GTC CCC GTC ACC CGA AAC GAC ATC GTG Trp Ile Lys Ser Gly Thr Leu Val Pro Val Thr Arg Asn Asp Ile Val	782	
10 225	230	235
AAG ATA GAA GGC ATC GAT GCC ACC GGC GGC AAT AAC CAG CCT AAC ATT Lys Ile Glu Gly Ile Asp Ala Thr Gly Gly Asn Asn Gln Pro Asn Ile	830	
15 240	245	250
CCG GAT ATC CCT GCG CAC CTA TGG TAC TTC GGG TTA ATT GGG ACA TGT Pro Asp Ile Pro Ala His Leu Trp Tyr Phe Gly Leu Ile Gly Thr Cys	878	
20 255	260	265
CTT TAGTGCGAAG CTT	894	
Leu		
25 270		

(2) INFORMATION FOR SEQ ID NO: 8:

30 (i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 270 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

40
 Ala Glu Val Ser Gln Asp Leu Phe Asn Gln Phe Asn Leu Phe Ala Gln
 1 5 10 15

 45 Tyr Ser Ala Aia Ala Tyr Cys Gly Lys Asn Asn Asp Ala Pro Ala Gly
 20 25 30

 50 Thr Asn Ile Thr Cys Thr Gly Asn Ala Cys Pro Glu Val Glu Lys Ala
 35 40 45

 55 Asp Ala Thr Phe Leu Tyr Ser Phe Glu Asp Ser Gly Val Gly Asp Val
 50 55 60

Thr Gly Phe Leu Ala Leu Asp Asn Thr Asn Lys Leu Ile Val Leu Ser
 65 70 75 80
 5
 Phe Arg Gly Ser Arg Ser Ile Glu Asn Trp Ile Gly Asn Leu Asn Phe
 85 90 95
 10
 Asp Leu Lys Glu Ile Asn Asp Ile Cys Ser Gly Cys Arg Gly His Asp
 100 105 110
 15
 Gly Phe Thr Ser Ser Trp Arg Ser Val Ala Asp Thr Leu Arg Gln Lys
 115 120 125
 20
 Val Glu Asp Ala Val Arg Glu His Pro Asp Tyr Arg Val Val Phe Thr
 130 135 140
 Gly His Ser Leu Gly Gly Ala Leu Ala Thr Val Ala Gly Ala Asp Leu
 145 150 155 160
 25
 Arg Gly Asn Gly Tyr Asp Ile Asp Val Phe Ser Tyr Gly Ala Pro Arg
 165 170 175
 30
 Val Gly Asn Arg Ala Phe Ala Glu Phe Leu Thr Val Gln Thr Gly Gly
 180 185 190
 35
 Thr Leu Tyr Arg Ile Thr His Thr Asn Asp Ile Val Pro Arg Leu Pro
 195 200 205
 Pro Arg Glu Phe Gly Tyr Ser His Ser Ser Pro Glu Tyr Trp Ile Lys
 210 215 220
 40
 Ser Gly Thr Leu Val Pro Val Thr Arg Asn Asp Ile Val Lys Ile Glu
 225 230 235 240
 45
 Gly Ile Asp Ala Thr Gly Gly Asn Asn Gln Pro Asn Ile Pro Asp Ile
 245 250 255
 Pro Ala His Leu Trp Tyr Phe Gly Leu Ile Gly Thr Cys Leu
 260 265 270
 50

(2) INFORMATION FOR SEQ ID NO: 9:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: primer

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATCCCTGCGC ACCTATGGTA CTTCCGGTTA ATTGGGACAT GTCTTGCTAG CCTTA

55

15 (2) INFORMATION FOR SEQ ID NO: 10:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: primer

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGCTTAAGGC TAGCAAGACA TGTCCCAATT AACCCGAAGT ACCATAGGTG CGCAGGGAT

59

35 (2) INFORMATION FOR SEQ ID NO: 11:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1828 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Geotrichum candidum
 (B) STRAIN: CMICC 335426

50 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 40..1731
 (D) OTHER INFORMATION: /product= "lipase"

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 (B) LOCATION: 40..96

5

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
 (B) LOCATION: 97..1728
 (D) OTHER INFORMATION: /product= "lipase" /gene= "lipB"

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

15	AATTCGGCAC GAGATTCCCTT TGATTTGCAA CTGTTAAC	ATG GTT TCC AAA AGC	54
		Met Val Ser Lys Ser	
		-19	-15
20	TTT TTT TTG GCT GCG GCG CTC AAC GTA GTG GGC ACC TTG GCC CAG GCC	Phe Phe Leu Ala Ala Ala Leu Asn Val Val Gly Thr Leu Ala Gln Ala	102
	-10	-5	1
25	CCC ACG GCC GTT CTT AAT GGC AAC GAG GTC ATC TCT GGT GTC CTT GAG	Pro Thr Ala Val Leu Asn Gly Asn Glu Val Ile Ser Gly Val Leu Glu	150
	5	10	15
30	GGC AAG GTT GAT ACC TTC AAG CGA ATC CCA TTT GCT GAC CCT CCT GTT	Gly Lys Val Asp Thr Phe Lys Gly Ile Pro Phe Ala Asp Pro Pro Val	198
	20	25	30
35	GGT GAC TTG CGG TTC AAG CAC CCC CAG CCT TTC ACT GGA TCC TAC CAG	Gly Asp Leu Arg Phe Lys His Pro Gln Pro Phe Thr Gly Ser Tyr Gln	246
	35	40	45
40	GGT CTT AAG GCC AAC GAC TTC AGC TCT GCT TGT ATG CAG CTT GAT CCT	Gly Leu Lys Ala Asn Asp Phe Ser Ser Ala Cys Met Gln Leu Asp Pro	294
	55	60	65

45

50

55

GGC AAT GCC TTT TCT TTG CTT GAC AAA GTA CTG GCC TTG GGA AAG ATT
 Gly Asn Ala Phe Ser Leu Leu Asp Lys Val Val Gly Leu Gly Lys Ile
 5 70 75 80

 CTT CCT GAT AAC CTT AGA GCC CCT CTT TAT GAC ATG GCC CAG GGT AGT
 Leu Pro Asp Asn Leu Arg Gly Pro Leu Tyr Asp Met Ala Gln Gly Ser
 10 85 90 95

 GTC TCC ATG AAT GAG GAC TGT CTC TAC CTT AAC GTT TTC CGC CCC GCT
 Val Ser Met Asn Glu Asp Cys Leu Tyr Leu Asn Val Phe Arg Pro Ala
 15 100 105 110

 GGC ACC AAG CCT GAT GCT AAG CTC CCC GTC ATG GTT TGG ATT TAC GGT
 Gly Thr Lys Pro Asp Ala Lys Leu Pro Val Met Val Trp Ile Tyr Gly
 20 115 120 125 130

 GGT GGC TTT GTG TTT GGT TCT TCT GCT TCT TAC CCT GCT AAC GGC TAC
 Gly Ala Phe Val Phe Gly Ser Ser Ala Ser Tyr Pro Gly Asn Gly Tyr
 25 135 140 145

 GTC AAG GAG AGT GTG GAA ATG GGC CAG CCT GTT GTG TTT GTT TCC ATC
 Val Lys Glu Ser Val Glu Met Gly Gln Pro Val Val Phe Val Ser Ile
 30 150 155 160

 AAC TAC CGT ACC CCC TAT GGA TTC TTG GGT GAT GCC ATC ACC
 Asn Tyr Arg Thr Gly Pro Tyr Gly Phe Leu Gly Asp Ala Ile Thr
 35 165 170 175

 GCT GAG GGC AAC ACC AAC GCT GGT CTG CAC GAC CAG CGC AAG GGT CTC
 Ala Glu Gly Asn Thr Asn Ala Gly Leu His Asp Gln Arg Lys Gly Leu
 40 180 185 190

 GAG TGG GTT AGC GAC AAC ATT GCC AAC TTT GGT GGT GAT CCC GAC AAG
 Glu Trp Val Ser Asp Asn Ile Ala Asn Phe Gly Gly Asp Pro Asp Lys
 45 195 200 205 210

 GTC ATG ATT TTC GGT GAG TCC GCT GGT GCC ATG AGT GTT GCT CAC CAG
 Val Met Ile Phe Gly Glu Ser Ala Gly Ala Met Ser Val Ala His Gln
 50 215 220 225

 CTT GTT GCC TAC GGT GGT GAC AAC ACC TAC AAC GGA AAG CAG CTT TTC
 Leu Val Ala Tyr Gly Gly Asp Asn Thr Tyr Asn Gly Lys Gln Leu Phe
 55 230 235 240

	CAC TCT GCC ATT CTT CAG TCT GGC GGT CCT CTT CCT TAC TTT GAC TCT		870
5	His Ser Ala Ile Leu Gln Ser Gly Gly Pro Leu Pro Tyr Phe Asp Ser		
	245	250	255
	ACT TCT GTT GGT CCC GAG AGT GCC TAC AGC AGA TTT GCT CAG TAT GCC		918
10	Thr Ser Val Gly Pro Glu Ser Ala Tyr Ser Arg Phe Ala Gln Tyr Ala		
	260	265	270
	GGA TGT GAC ACC AGT GCC AGT GAT AAT GAC ACT CTG GCT TGT CTC CGC		966
15	Gly Cys Asp Thr Ser Ala Ser Asp Asn Asp Thr Leu Ala Cys Leu Arg		
	275	280	285
	AGC AAG TCC AGC GAT GTC TTG CAC AGT GCG CAG AAC TCG TAT GAT CTT		1014
20	Ser Lys Ser Ser Asp Val Leu His Ser Ala Gln Asn Ser Tyr Asp Leu		
	295	300	305
	AAG GAC CTG TTT GGT CTG CTC CCT CAA TTC CTT GGA TTT GGT CCC AGA		1062
25	Lys Asp Leu Phe Gly Leu Leu Pro Gln Phe Leu Gly Phe Gly Pro Arg		
	310	315	320
	CCC GAC GGC AAC ATT ATT CCC GAT GCC GCT TAT GAG CTC TAC CGC AGC		1110
30	Pro Asp Gly Asn Ile Ile Pro Asp Ala Ala Tyr Glu Leu Tyr Arg Ser		
	325	330	335
	GGT AGA TAC GCC AAG GTT CCC TAC ATT ACT GGC AAC CAG CAG GAT GAG		1158
35	Gly Arg Tyr Ala Lys Val Pro Tyr Ile Thr Gly Asn Gln Glu Asp Glu		
	340	345	350
	GGT ACT ATT CTT GCC CCC GTT GCT ATT AAT GCT ACC ACT ACT CCC CAT		1206
40	Gly Thr Ile Leu Ala Pro Val Ala Ile Asn Ala Thr Thr Thr Pro His		
	355	360	365
	GTT AAG AAG TGG TTG AAG TAC ATT TGT AGC CAG GCT TCT GAC GCT TCG		1254
45	Val Lys Lys Trp Leu Lys Tyr Ile Cys Ser Gln Ala Ser Asp Ala Ser		
	375	380	385
	CTT GAT CGT GTT TTG TCG CTC TAC CCC GGC TCT TGG TCG GAG GGT TCA		1302
50	Leu Asp Arg Val Leu Ser Leu Tyr Pro Gly Ser Trp Ser Glu Gly Ser		
	390	395	400
	CCA TTC CGC ACT GGT ATT CTT AAT GCT CTT ACC CCT CAG TTC AAG CGC		1350
55	Pro Phe Arg Thr Gly Ile Leu Asn Ala Leu Thr Pro Gln Phe Lys Arg		
	405	410	415

	ATT GCT CCC ATT TTC ACT GAT TTG CTG TTC CAG TCT CCT CGT CGT GTT Ile Ala Ala Ile Phe Thr Asp Leu Leu Phe Gln Ser Pro Arg Arg Val	1398
5	420 425 430	
	ATG CTT AAC GCT ACC AAG GAC GTC AAC CGC TGG ACT TAC CTT GCC ACC Met Leu Asn Ala Thr Lys Asp Val Asn Arg Trp Thr Tyr Leu Ala Thr	1446
10	435 440 445 450	
	CAG CTC CAT AAC CTC GTT CCA TTT TTG GGT ACT TTC CAT GGC AGT GAT Gln Leu His Asn Leu Val Pro Phe Leu Gly Thr Phe His Gly Ser Asp	1494
15	455 460 465	
	CTT CTT TTT CAA TAC TAC GTG GAC CTT GGC CCA TCT TCT GCT TAC CGC Leu Leu Phe Gln Tyr Tyr Val Asp Leu Gly Pro Ser Ser Ala Tyr Arg	1542
20	470 475 480	
	CGC TAC TTT ATC TCG TTT GCC AAC CAC CAC GAC CCC AAC GTT GGT ACC Arg Tyr Phe Ile Ser Phe Ala Asn His His Asp Pro Asn Val Gly Thr	1590
25	485 490 495	
	AAC CTC CAA CAG TGG GAT ATG TAC ACT GAT GCA GGC AAG GAG ATG CTT Asn Leu Gln Gln Trp Asp Met Tyr Thr Asp Ala Gly Lys Glu Met Leu	1638
30	500 505 510	
	CAG ATT CAT ATG ATT GGT AAC TCT ATG AGA ACT GAC GAC TTT AGA ATC Gln Ile His Met Ile Gly Asn Ser Met Arg Thr Asp Asp Phe Arg Ile	1686
35	515 520 525 530	
	GAG GGA ATC TCG AAC TTT GAG TCT GAC GTT ACT CTC TTC GGT TAATCCCATT Glu Gly Ile Ser Asn Phe Glu Ser Asp Val Thr Leu Phe Gly	1738
40	535 540 545	
	TAGCAAGTTT TGTGTATTTA AAGTATACCA GTTGATGTAA TATATCAATA GATTACAAT	1798
	TAATTTAGTGA AAAAAAAAAA AAAAAAAAAC	1828
45		

(2) INFORMATION FOR SEQ ID NO: 12:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 563 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Val Ser Lys Ser Phe Phe Leu Ala Ala Ala Leu Asn Val Val Gly
 -19 -15 -10 -5

5 Thr Leu Ala Gln Ala Pro Thr Ala Val Leu Asn Gly Asn Glu Val Ile
 1 5 10

10 Ser Gly Val Leu Glu Gly Lys Val Asp Thr Phe Lys Gly Ile Pro Phe
 15 20 25

15 Ala Asp Pro Pro Val Gly Asp Leu Arg Phe Lys His Pro Gln Pro Phe
 30 35 40 45

20 Thr Gly Ser Tyr Gln Gly Leu Lys Ala Asn Asp Phe Ser Ser Ala Cys
 50 55 60

25 Met Gln Leu Asp Pro Gly Asn Ala Phe Ser Leu Leu Asp Lys Val Val
 65 70 75

30 Gly Leu Gly Lys Ile Leu Pro Asp Asn Leu Arg Gly Pro Leu Tyr Asp
 80 85 90

35 Met Ala Gln Gly Ser Val Ser Met Asn Glu Asp Cys Leu Tyr Leu Asn
 95 100 105

40 Val Phe Arg Pro Ala Gly Thr Lys Pro Asp Ala Lys Leu Pro Val Met
 110 115 120 125

45 Val Trp Ile Tyr Gly Gly Ala Phe Val Phe Gly Ser Ser Ala Ser Tyr
 130 135 140

50 Pro Gly Asn Gly Tyr Val Lys Glu Ser Val Glu Met Gly Gln Pro Val
 145 150 155

55 Val Phe Val Ser Ile Asn Tyr Arg Thr Gly Pro Tyr Gly Phe Leu Gly
 160 165 170

Gly Asp Ala Ile Thr Ala Glu Gly Asn Thr Asn Ala Gly Leu His Asp
 175 180 185

60 Gln Arg Lys Gly Leu Glu Trp Val Ser Asp Asn Ile Ala Asn Phe Gly
 190 195 200 205

55

Gly Asp Pro Asp Lys Val Met Ile Phe Gly Glu Ser Ala Gly Ala Met
 210 215 220
 5 Ser Val Ala His Gln Leu Val Ala Tyr Gly Gly Asn Thr Tyr Asn
 225 230 235
 10 Gly Lys Gln Leu Phe His Ser Ala Ile Leu Gln Ser Gly Gly Pro Leu
 240 245 250
 15 Pro Tyr Phe Asp Ser Thr Ser Val Gly Pro Glu Ser Ala Tyr Ser Arg
 255 260 265
 20 Phe Ala Gln Tyr Ala Gly Cys Asp Thr Ser Ala Ser Asp Asn Asp Thr
 270 275 280 285
 25 Leu Ala Cys Leu Arg Ser Lys Ser Ser Asp Val Leu His Ser Ala Gln
 290 295 300
 30 Asn Ser Tyr Asp Leu Lys Asp Leu Phe Gly Leu Leu Pro Gln Phe Leu
 305 310 315
 35 Gly Phe Gly Pro Arg Pro Asp Gly Asn Ile Ile Pro Asp Ala Ala Tyr
 320 325 330
 40 Glu Leu Tyr Arg Ser Gly Arg Tyr Ala Lys Val Pro Tyr Ile Thr Gly
 335 340 345
 45 Asn Gln Glu Asp Glu Gly Thr Ile Leu Ala Pro Val Ala Ile Asn Ala
 350 355 360 365
 50 Thr Thr Thr Pro His Val Lys Lys Trp Leu Lys Tyr Ile Cys Ser Gln
 370 375 380
 Ala Ser Asp Ala Ser Leu Asp Arg Val Leu Ser Leu Tyr Pro Gly Ser
 385 390 395
 55 Trp Ser Glu Gly Ser Pro Phe Arg Thr Gly Ile Leu Asn Ala Leu Thr
 400 405 410
 Pro Gln Phe Lys Arg Ile Ala Ala Ile Phe Thr Asp Leu Leu Phe Gln
 415 420 425
 Ser Pro Arg Arg Val Met Leu Asn Ala Thr Lys Asp Val Asn Arg Trp
 430 435 440 445

Thr Tyr Leu Ala Thr Gln Leu. His Asn Leu Val Pro Phe Leu Gly Thr
450 455 460

5

Phe His Gly Ser Asp Leu Leu Phe Gln Tyr Tyr Val Asp Leu Gly Pro
465 470 475

10

Ser Ser Ala Tyr Arg Arg Tyr Phe Ile Ser Phe Ala Asn His His Asp
480 485 490

15

Pro Asn Val Gly Thr Asn Leu Gln Gln Trp Asp Met Tyr Thr Asp Ala
495 500 505

30

Gly Lys Glu Met Leu Gln Ile His Met Ile Gly Asn Ser Met Arg Thr
510 515 520 525

20

Asp Asp Phe Arg Ile Glu Gly Ile Ser Asn Phe Glu Ser Asp Val Thr

5

Leu Phe Gly

(2) INFORMATION FOR SEQ ID NO: 13:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

40

(vii) IMMEDIATE SOURCE:

(B) CLONE: primer lipo3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

45

GGGGCGGGCCG CGCAGGGCCC AAGGCGGTCT CTCAAT

36

50

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

5 (B) CLONE: Part non-coding strand lipasell

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

10 **ATTGAGAGAC CGCCGTGGGG CCTGGGCCAG**

30

(2) INFORMATION FOR SEQ ID NO: 15:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

25 (vii) IMMEDIATE SOURCE:

25 (B) CLONE: Part coding strand lipasell

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

30 **CAAACTTTGA GACTGACGTT AATCTCTACG CTAAAAC**

38

(2) INFORMATION FOR SEQ ID NO: 16:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: DNA (genomic)

45 (vii) IMMEDIATE SOURCE:

(B) CLONE: primer lipo4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

50 **CCCCGCTAGC ACCGTAGAGA TTAACGTCAG TC**

32

55 (2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

10

(B) CLONE: primer lipo5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

15

CCCGCGGCCG CGAGCATTGA TGGTGGTATC**30**

(2) INFORMATION FOR SEQ ID NO: 18:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

30

(B) CLONE: Part non-coding strand lipase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

35

GATACCACGA TCAATGCT**18**

40

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(vii) IMMEDIATE SOURCE:

55

(B) CLONE: Part coding strand lipase

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AACACAGGCC TCTGTACT**18**5 **(2) INFORMATION FOR SEQ ID NO: 20:**

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (vii) IMMEDIATE SOURCE:

(B) CLONE: primer lipo6

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

CCGCGCTAGC AGTACAGAGG CCTGTGTT**28**25 **(2) INFORMATION FOR SEQ ID NO: 21:**

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 2685 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Saccharomyces cerevisiae*

40 (vii) IMMEDIATE SOURCE:

(B) CLONE: pYY105

45 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 1..2685
 (D) OTHER INFORMATION: /product= "Flocculation protein" /gene= "FLO1"

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

55

	ATG ACA ATG CCT CAT CGC TAT ATG TTT TTG GCA GTC TTT ACA CTT CTG		48
5	Met Thr Met Pro His Arg Tyr Met Phe Leu Ala Val Phe Thr Leu Leu		
	1 5 10 15		
	GCA CTA ACT AGT GTG GCC TCA GGA GCC ACA GAG GCG TGC TTA CCA GCA		96
10	Ala Leu Thr Ser Val Ala Ser Gly Ala Thr Glu Ala Cys Leu Pro Ala		
	20 25 30		
15	GCC CAG AGG AAA AGT GGG ATG AAT ATA AAT TTT TAC CAG TAT TCA TTG		144
	Gly Gln Arg Lys Ser Gly Met Asn Ile Asn Phe Tyr Gln Tyr Ser Leu		
	35 40 45		
20	AAA GAT TCC TCC ACA TAT TCG AAT GCA GCA TAT ATG GCT TAT GGA TAT		192
	Lys Asp Ser Ser Thr Tyr Ser Asn Ala Ala Tyr Met Ala Tyr Gly Tyr		
	50 55 60		
25	GCC TCA AAA ACC AAA CTA GGT TCT GTC GGA CGA CAA ACT GAT ATC TCG		240
	Ala Ser Lys Thr Lys Leu Gly Ser Val Gly Gly Gln Thr Asp Ile Ser		
	65 70 75 80		
30	ATT GAT TAT AAT ATT CCC TGT GTT AGT TCA TCA CGC ACA TTT CCT TGT		288
	Ile Asp Tyr Asn Ile Pro Cys Val Ser Ser Gly Thr Phe Pro Cys		
	85 90 95		
35	CCT CAA GAA GAT TCC TAT GGA AAC TGG GGA TGC AAA GGA ATG GGT GCT		336
	Pro Gln Glu Asp Ser Tyr Gly Asn Trp Gly Cys Lys Gly Met Gly Ala		
	100 105 110		
40	TGT TCT AAT AGT CAA CGA ATT GCA TAC TGG AGT ACT GAT TTA TTT GGT		384
	Cys Ser Asn Ser Gln Gly Ile Ala Tyr Trp Ser Thr Asp Leu Phe Gly		
	115 120 125		
45			
50			
55			

	TTC TAT ACT ACC CCA ACA AAC GTA ACC CTA GAA ATG ACA GGT TAT TTT Phe Tyr Thr Thr Pro Thr Asn Val Thr Leu Glu Met Thr Gly Tyr Phe 130 135 140	432
5		
10	TTA CCA CCA CAG ACG GGT TCT TAC ACA TTC AAG TTT GCT ACA GTT GAC Leu Pro Pro Gln Thr Gly Ser Tyr Thr Phe Lys Phe Ala Thr Val Asp 145 150 155 160	480
15		
20	GAC TCT GCA ATT CTA TCA GTA GGT GCA ACC GCG TTC AAC TGT TGT Asp Ser Ala Ile Leu Ser Val Gly Gly Ala Thr Ala Phe Asn Cys Cys 165 170 175	528
25		
30	GCT CAA CAG CAA CCG CCG ATC ACA TCA ACG AAC TTT ACC ATT GAC GGT Ala Gln Gln Gln Pro Pro Ile Thr Ser Thr Asn Phe Thr Ile Asp Gly 180 185 190	576
35		
40	ATC AAG CCA TGG GGT GGA AGT TTG CCA CCT AAT ATC GAA GGA ACC GTC Ile Lys Pro Trp Gly Gly Ser Leu Pro Pro Asn Ile Glu Gly Thr Val 195 200 205	624
45		
50	TAT ATG TAC GCT GGC TAC TAT TAT CCA ATG AAG GTT GTT TAC TCG AAC Tyr Met Tyr Ala Gly Tyr Tyr Pro Met Lys Val Val Tyr Ser Asn 210 215 220	672
55		
60	GCT GTT TCT TGG GGT ACA CTT CCA ATT AGT GTG ACA CTT CCA GAT GGT Ala Val Ser Trp Gly Thr Leu Pro Ile Ser Val Thr Leu Pro Asp Gly 225 230 235 240	720
65		
70	ACC ACT GTA ACT GAT GAC TTC GAA GGG TAC GTC TAT TCC TTT GAC GAT Thr Thr Val Ser Asp Asp Phe Glu Gly Tyr Val Tyr Ser Phe Asp Asp 245 250 255	768
75		
80	GAC CTA AGT CAA TCT AAC TGT ACT GTC CCT GAC CCT TCA AAT TAT GCT Asp Leu Ser Gln Ser Asn Cys Thr Val Pro Asp Pro Ser Asn Tyr Ala 260 265 270	816
85		
90	GTC AGT ACC ACT ACA ACT ACA ACG GAA CCA TGG ACC GGT ACT TTC ACT Val Ser Thr Thr Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr 275 280 285	864
95		
100	TCT ACA TCT ACT GAA ATG ACC ACC GTC ACC GGT ACC AAC GGC GTT CCA Ser Thr Ser Thr Glu Met Thr Thr Val Thr Gly Thr Asn Gly Val Pro 290 295 300	912

	ACT GAC GAA ACC GTC ATT GTC ATC AGA ACT CCA ACC AGT GAA GGT CTA		960	
5	Thr Asp Glu Thr Val Ile Val Ile Arg Thr Pro Thr Ser Glu Gly Leu			
	305	310	315	320
	ATC AGC ACC ACC ACT GAA CCA TGG ACT GGC ACT TTC ACT TCG ACT TCC		1008	
10	Ile Ser Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser			
	325	330	335	
	ACT GAG GTT ACC ACC ATC ACT GGA ACC AAC GGT CAA CCA ACT GAC GAA		1056	
15	Thr Glu Val Thr Thr Ile Thr Gly Thr Asn Gly Gln Pro Thr Asp Glu			
	340	345	350	
	ACT GTG ATT GTT ATC AGA ACT CCA ACC AGT GAA GGT CTA ATC ACC ACC		1104	
	Thr Val Ile Val Ile Arg Thr Pro Thr Ser Glu Gly Leu Ile Ser Thr			
20	355	360	365	
	ACC ACT GAA CCA TGG ACT GGT ACT TTC ACT TCT ACA TCT ACT GAA ATG		1152	
	Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser Thr Glu Met			
25	370	375	380	
	ACC ACC GTC ACC GGT ACT AAC GGT CAA CCA ACT GAC GAA ACC GTG ATT		1200	
	Thr Thr Val Thr Gly Thr Asn Gly Gln Pro Thr Asp Glu Thr Val Ile			
30	385	390	395	400
	GTT ATC AGA ACT CCA ACC AGT GAA CGT TTG GTT ACA ACC ACC ACT GAA		1248	
	Val Ile Arg Thr Pro Thr Ser Glu Gly Leu Val Thr Thr Thr Glu			
	405	410	415	
35	CCA TGG ACT GGT ACT TTT ACT TCG ACT TCC ACT GAA ATG TCT ACT GTC		1296	
	Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser Thr Glu Met Ser Thr Val			
	420	425	430	
40	ACT GGA ACC AAT GGC TTG CCA ACT GAT GAA ACT GTC ATT GTT GTC AAA		1344	
	Thr Gly Thr Asn Gly Leu Pro Thr Asp Glu Thr Val Ile Val Val Lys			
	435	440	445	
45	ACT CCA ACT ACT GCC ATC TCA TCC ACT TTG TCA TCA TCA TCT TCA GGA		1392	
	Thr Pro Thr Thr Ala Ile Ser Ser Ser Leu Ser Ser Ser Ser Gly			
	450	455	460	
50	CAA ATC ACC AGC TCT ATC ACG TCT TCG CGT CCA ATT ATT ACC CCA TTC		1440	
	Gln Ile Thr Ser Ser Ile Thr Ser Ser Arg Pro Ile Ile Thr Pro Phe			
	465	470	475	480

	TAT CCT AGC AAT GGA ACT TCT GTG ATT TCT TCC TCA GTA ATT TCT TCC		1488
	Tyr Pro Ser Asn Gly Thr Ser Val Ile Ser Ser Ser Val Ile Ser Ser		
5	485	490	495
	TCA GTC ACT TCT TCT CTA TTC ACT TCT TCT CCA GTC ATT TCT TCC TCA		1536
	Ser Val Thr Ser Ser Leu Phe Thr Ser Ser Pro Val Ile Ser Ser Ser		
10	500	505	510
	GTC ATT TCT TCT ACA ACA ACC TCC ACT TCT ATA TTT TCT GAA TCA		1584
	Val Ile Ser Ser Ser Thr Thr Ser Thr Ser Ile Phe Ser Glu Ser		
15	515	520	525
	TCT AAA TCA TCC GTC ATT CCA ACC AGT AGT TCC ACC TCT GGT TCT TCT		1632
	Ser Lys Ser Ser Val Ile Pro Thr Ser Ser Ser Thr Ser Gly Ser Ser		
20	530	535	540
	GAG AGC GAA ACG AGT TCA GCT GGT TCT GTC TCT TCC TCT TTT ATC		1680
	Glu Ser Glu Thr Ser Ser Ala Gly Ser Val Ser Ser Ser Phe Ile		
25	545	550	555
	TCT TCT GAA TCA TCA AAA TCT CCT ACA TAT TCT TCT TCA TCA TTA CCA		1728
	Ser Ser Glu Ser Ser Lys Ser Pro Thr Tyr Ser Ser Ser Ser Leu Pro		
30	565	570	575
	CTT GTT ACC AGT GCG ACA ACA AGC CAG GAA ACT GCT TCT TCA TTA CCA		1776
	Leu Val Thr Ser Ala Thr Thr Ser Gln Glu Thr Ala Ser Ser Leu Pro		
35	580	585	590
	CCT GCT ACC ACT ACA AAA ACG AGC GAA CAA ACC ACT TTG GTT ACC GTG		1824
	Pro Ala Thr Thr Lys Thr Ser Glu Gln Thr Thr Leu Val Thr Val		
40	595	600	605
	ACA TCC TCC GAG TCT CAT GTG TGC ACT GAA TCC ATC TCC CCT GCG ATT		1872
	Thr Ser Cys Glu Ser His Val Cys Thr Glu Ser Ile Ser Pro Ala Ile		
45	610	615	620
	GTT TCC ACA GCT ACT GTT ACT GTT AGC GGC GTC ACA ACA GAG TAT ACC		1920
	Val Ser Thr Ala Thr Val Thr Val Ser Gly Val Thr Thr Glu Tyr Thr		
50	625	630	635
	ACA TGG TCC CCT ATT TCT ACT ACA GAG ACA ACA AAG CAA ACC AAA GGG		1968
	Thr Trp Cys Pro Ile Ser Thr Thr Glu Thr Thr Lys Gln Thr Lys Gly		
55	645	650	655

	ACA ACA GAG CAA ACC ACA GAA ACA ACA AAA CAA ACC ACG GTA GTT ACA Thr Thr Glu Gln Thr Thr Glu Thr Thr Lys Gln Thr Thr Val Val Thr	2016
5	660 665 670	
	ATT TCT TCT TGT GAA TCT GAC GTA TGC TCT AAG ACT GCT TCT CCA GCC Ile Ser Ser Cys Glu Ser Asp Val Cys Ser Lys Thr Ala Ser Pro Ala	2064
10	675 680 685	
	ATT GTA TCT ACA AGC ACT GCT ACT ATT AAC CGC GTT ACT ACA GAA TAC Ile Val Ser Thr Ser Thr Ala Thr Ile Asn Gly Val Thr Thr Glu Tyr	2112
15	690 695 700	
	ACA ACA TGG TGT CCT ATT TCC ACC ACA GAA TCG AGG CAA CAA ACA ACG Thr Thr Trp Cys Pro Ile Ser Thr Thr Glu Ser Arg Gln Gln Thr Thr	2160
20	705 710 715 720	
	CTA GTT ACT GTT ACT TCC TGC GAA TCT GGT GTG TGT TCC GAA ACT GCT Leu Val Thr Val Thr Ser Cys Glu Ser Gly Val Cys Ser Glu Thr Ala	2208
25	725 730 735	
	TCA CCT GCC ATT GTT TCG ACG GCC ACG GCT ACT GTG AAT GAT GTT GTT Ser Pro Ala Ile Val Ser Thr Ala Thr Ala Thr Val Asn Asp Val Val	2256
30	740 745 750	
	ACG GTC TAT CCT ACA TGG AGG CCA CAG ACT GCG AAT GAA GAG TCT GTC Thr Val Tyr Pro Thr Trp Arg Pro Gln Thr Ala Asn Glu Glu Ser Val	2304
35	755 760 765	
	AGC TCT AAA ATG AAC AGT GCT ACC GGT GAG ACA ACA ACC AAT ACT TTA Ser Ser Lys Met Asn Ser Ala Thr Gly Glu Thr Thr Asn Thr Leu	2352
40	770 775 780	
	GCT GCT GAA ACG ACT ACC AAT ACT GTA GCT GCT GAG ACG ATT ACC AAT Ala Ala Glu Thr Thr Asn Thr Val Ala Ala Glu Thr Ile Thr Asn	2400
45	785 790 795 800	
	ACT GGA GCT GCT GAG ACG AAA ACA GTA GTC ACC TCT TCG CTT TCA AGA Thr Gly Ala Ala Glu Thr Lys Thr Val Val Thr Ser Ser Leu Ser Arg	2448
50	805 810 815	
	TCT AAT CAC GCT GAA ACA CAG ACG GCT TCC GCG ACC GAT GTG ATT GGT Ser Asn His Ala Glu Thr Gln Thr Ala Ser Ala Thr Asp Val Ile Gly	2496
55	820 825 830	

CAC AGC AGT AGT GTT TCT GTA TCC GAA ACT GGC AAC ACC AAG AGT His Ser Ser Ser Val Val Ser Val Ser Glu Thr Gly Asn Thr Lys Ser	2544
5 835 840 845	
CTA ACA AGT TCC GGG TTG AGT ACT ATG TCG CAA CAG CCT CGT AGC ACA Leu Thr Ser Ser Gly Leu Ser Thr Met Ser Gln Gln Pro Arg Ser Thr	2592
10 850 855 860	
CCA GCA AGC AGC ATG GTA GGA TAT AGT ACA GCT TCT TTA GAA ATT TCA Pro Ala Ser Ser Met Val Gly Tyr Ser Thr Ala Ser Leu Glu Ile Ser	2640
15 865 870 875 880	
ACG TAT GCT GGC AGT GCA ACA GCT TAC TGG CCG GTA GTG GTT TAA Thr Tyr Ala Gly Ser Ala Thr Ala Tyr Trp Pro Val Val Val	2686
20 885 890 895	

(2) INFORMATION FOR SEQ ID NO: 22:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 894 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Met Thr Met Pro His Arg Tyr Met Phe Leu Ala Val Phe Thr Leu Leu 1 5 10 15	
40 Ala Leu Thr Ser Val Ala Ser Gly Ala Thr Glu Ala Cys Leu Pro Ala 20 25 30	
45 Gly Gln Arg Lys Ser Gly Met Asn Ile Asn Phe Tyr Gln Tyr Ser Leu 35 40 45	
50 Lys Asp Ser Ser Thr Tyr Ser Asn Ala Ala Tyr Met Ala Tyr Gly Tyr 50 55 60	
55 Ala Ser Lys Thr Lys Leu Gly Ser Val Gly Gly Gln Thr Asp Ile Ser 65 70 75 80	
55 Ile Asp Tyr Asn Ile Pro Cys Val Ser Ser Gly Thr Phe Pro Cys 85 90 95	

Pro Gln Glu Asp Ser Tyr Gly Asn Trp Gly Cys Lys Gly Met Gly Ala
 100 105. 110
 5

Cys Ser Asn Ser Gln Gly Ile Ala Tyr Trp Ser Thr Asp Leu Phe Gly
 115 120 125

10 Phe Tyr Thr Thr Pro Thr Asn Val Thr Leu Glu Met Thr Gly Tyr Phe
 130 135 140

15 Leu Pro Pro Gln Thr Gly Ser Tyr Thr Phe Lys Phe Ala Thr Val Asp
 145 150 155 160

20 Asp Ser Ala Ile Leu Ser Val Gly Gly Ala Thr Ala Phe Asn Cys Cys
 165 170 175

25 Ala Gln Gln Gln Pro Pro Ile Thr Ser Thr Asn Phe Thr Ile Asp Gly
 180 185 190

Ile Lys Pro Trp Gly Gly Ser Leu Pro Pro Asn Ile Glu Gly Thr Val
 195 200 205

30 Tyr Met Tyr Ala Gly Tyr Tyr Tyr Pro Met Lys Val Val Tyr Ser Asn
 210 215 220

Ala Val Ser Trp Gly Thr Leu Pro Ile Ser Val Thr Leu Pro Asp Gly
 225 230 235 240

35 Thr Thr Val Ser Asp Asp Phe Glu Gly Tyr Val Tyr Ser Phe Asp Asp
 245 250 255

40 Asp Leu Ser Gln Ser Asn Cys Thr Val Pro Asp Pro Ser Asn Tyr Ala
 260 265 270

45 Val Ser Thr Thr Thr Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr
 275 280 285

Ser Thr Ser Thr Glu Met Thr Thr Val Thr Gly Thr Asn Gly Val Pro
 290 295 300

50 Thr Asp Glu Thr Val Ile Val Ile Arg Thr Pro Thr Ser Glu Gly Leu
 305 310 315 320

55 Ile Ser Thr Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser
 325 330 335

Thr Glu Val Thr Thr Ile Thr Gly Thr Asn Gly Gln Pro Thr Asp Glu
 340 345 350

5 Thr Val Ile Val Ile Arg Thr Pro Thr Ser Glu Gly Leu Ile Ser Thr
 355 360 365

10 Thr Thr Glu Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser Thr Glu Met
 370 375 380

15 Thr Thr Val Thr Gly Thr Asn Gly Gln Pro Thr Asp Glu Thr Val Ile
 385 390 395 400

20 Val Ile Arg Thr Pro Thr Ser Glu Gly Leu Val Thr Thr Thr Glu
 405 410 415

25 Pro Trp Thr Gly Thr Phe Thr Ser Thr Ser Thr Glu Met Ser Thr Val
 420 425 430

30 Thr Gly Thr Asn Gly Leu Pro Thr Asp Glu Thr Val Ile Val Val Lys
 435 440 445

35 Thr Pro Thr Thr Ala Ile Ser Ser Ser Leu Ser Ser Ser Ser Gly
 450 455 460

40 Gln Ile Thr Ser Ser Ile Thr Ser Ser Arg Pro Ile Ile Thr Pro Phe
 465 470 475 480

45 Tyr Pro Ser Asn Gly Thr Ser Val Ile Ser Ser Ser Val Ile Ser Ser
 485 490 495

50 Ser Val Thr Ser Ser Leu Phe Thr Ser Ser Pro Val Ile Ser Ser Ser
 500 505 510

55 Val Ile Ser Ser Ser Thr Thr Ser Thr Ser Ile Phe Ser Glu Ser
 515 520 525

60 Ser Lys Ser Ser Val Ile Pro Thr Ser Ser Ser Thr Ser Gly Ser Ser
 530 535 540

65 Glu Ser Glu Thr Ser Ser Ala Gly Ser Val Ser Ser Ser Phe Ile
 545 550 555 560

70 Ser Ser Glu Ser Ser Lys Ser Pro Thr Tyr Ser Ser Ser Ser Leu Pro
 565 570 575

Leu Val Thr Ser Ala Thr Thr Ser Gln Glu Thr Ala Ser Ser Leu Pro
 580 585 590
 5

Pro Ala Thr Thr Thr Lys Thr Ser Glu Gln Thr Thr Leu Val Thr Val
 595 600 605
 10

Thr Ser Cys Glu Ser His Val Cys Thr Glu Ser Ile Ser Pro Ala Ile
 610 615 620
 15

Val Ser Thr Ala Thr Val Thr Val Ser Gly Val Thr Thr Glu Tyr Thr
 625 630 635 640

Thr Trp Cys Pro Ile Ser Thr Thr Glu Thr Thr Lys Gln Thr Lys Gly
 645 650 655
 20

Thr Thr Glu Gln Thr Thr Glu Thr Thr Lys Gln Thr Thr Val Val Thr
 660 665 670

Ile Ser Ser Cys Glu Ser Asp Val Cys Ser Lys Thr Ala Ser Pro Ala
 675 680 685
 25

Ile Val Ser Thr Ser Thr Ala Thr Ile Asn Gly Val Thr Thr Glu Tyr
 690 695 700
 30

Thr Thr Trp Cys Pro Ile Ser Thr Thr Glu Ser Arg Gln Gln Thr Thr
 705 710 715 720

35

Leu Val Thr Val Thr Ser Cys Glu Ser Gly Val Cys Ser Glu Thr Ala
 725 730 735

Ser Pro Ala Ile Val Ser Thr Ala Thr Ala Thr Val Asn Asp Val Val
 740 745 750
 40

Thr Val Tyr Pro Thr Trp Arg Pro Gln Thr Ala Asn Glu Glu Ser Val
 755 760 765
 45

Ser Ser Lys Met Asn Ser Ala Thr Gly Glu Thr Thr Asn Thr Leu
 770 775 780

50

Ala Ala Glu Thr Thr Thr Asn Thr Val Ala Ala Glu Thr Ile Thr Asn
 785 790 795 800

Thr Gly Ala Ala Glu Thr Lys Thr Val Val Thr Ser Ser Leu Ser Arg
 805 810 815
 55

Ser Asn His Ala Glu Thr Gln Thr Ala Ser Ala Thr Asp Val Ile Gly
 5 820 825 830

His Ser Ser Ser Val Val Ser Val Ser Glu Thr Gly Asn Thr Lys Ser
 10 835 840 845

Leu Thr Ser Ser Gly Leu Ser Thr Met Ser Gln Gln Pro Arg Ser Thr
 850 855 860

Pro Ala Ser Ser Met Val Gly Tyr Ser Thr Ala Ser Leu Glu Ile Ser
 15 865 870 875 880

Thr Tyr Ala Gly Ser Ala Thr Ala Tyr Trp Pro Val Val Val
 20 885 890

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: primer pcrflol

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

40 GAATTCTGCTA GCAATTATGC TGTCAGTACC

30

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: Part non-coding sequence FLO1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

5 **AGTGGTACTG ACAGCATAAT TTGA****24**

(2) INFORMATION FOR SEQ ID NO: 25:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

20

(B) CLONE: Part coding sequence FLO1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

25

AATAAAATTC GCGTTCTTT TACG**24**

(2) INFORMATION FOR SEQ ID NO: 26:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: DNA (genomic)

40

(vii) IMMEDIATE SOURCE:

(B) CLONE: primer pcrflo2

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GAGCTCAAGC TTCGTAAAAA GAACGCGAAT T**31**50 **Claims**

1. Use of a lower eukaryote selected from the group consisting of yeasts and fungi containing an expressible first polynucleotide comprising a structural gene encoding a protein providing catalytic activity, said protein being immobilised at the exterior of the cell wall of said lower eukaryote, and at least part of a gene encoding an anchoring protein capable of anchoring in the cell wall of said lower eukaryote, said part encoding at least the anchoring part of said anchoring protein, which anchoring part is derivable from the C-terminal half of said anchoring protein, said first polynucleotide being present in either a vector or in a chromosome of said lower eukaryote, for carrying out an enzymatic process, by contacting a substrate for the protein providing catalytic activity, with the lower eukaryote.

2. Use according to claim 1 wherein the lower eukaryote is selected from the group consisting of yeasts belonging to the genera *Candida*, *Debaryomyces*, *Hansenula*, *Kluyveromyces*, *Pichia* and *Saccharomyces* and fungi belonging to the genera *Aspergillus*, *Penicillium* and *Rhizopus* can be used.
- 5 3. Use according to claim 1 or 2 wherein the protein capable of anchoring in the cell wall is selected from the group consisting of, AGA1 (=α-agglutinin) of *S. cerevisiae*, FLO1 (= flocculation protein), Major Cell Wall Protein of lower eukaryotes, selected from the group consisting of yeasts and fungi.
- 10 4. Use according to any of claims 1-3 wherein the protein providing catalytic activity is selected from the group consisting of hydrolytic enzymes including lipases and oxidoreductases including oxidases.
- 15 5. Use according to claim 1 wherein said lower eukaryote further comprises a sequence encoding a signal peptide ensuring secretion of the expression product of said first polynucleotide.
- 20 6. Use according to claim 5, wherein the protein providing catalytic activity exhibits said catalytic activity when present in a multimeric form, said lower eukaryote further comprising a second polynucleotide comprising a structural gene encoding the same protein providing catalytic activity combined with a sequence encoding a signal peptide ensuring secretion of the expression product of said second polynucleotide, said second polynucleotide being operably linked to a regulatable promoter.

Revendications

- 25 1. Utilisation d'un eucaryote inférieur choisi dans l'ensemble comprenant les levures et les champignons, contenant un premier polynucléotide exprimable comprenant un gène de structure codant pour une protéine assurant une activité catalytique, ladite protéine étant immobilisée à l'extérieur de la paroi cellulaire dudit eucaryote inférieur, et au moins une partie d'un gène codant pour une protéine d'ancrage capable de s'ancrer dans la paroi cellulaire dudit eucaryote inférieur, ladite partie codant pour au moins la partie d'ancrage de ladite protéine d'ancrage, ledit premier polynucléotide étant présent dans un vecteur ou dans un chromosome dudit eucaryote inférieur, pour mettre en oeuvre un procédé enzymatique, par mise en contact, avec l'eucaryote inférieur, d'un substrat pour la protéine assurant l'activité catalytique.
- 30 2. Utilisation selon la revendication 1, pour laquelle l'eucaryote inférieur est choisi dans l'ensemble comprenant les levures appartenant aux genres *Candida*, *Debaryomyces*, *Hansenula*, *Kluyveromyces*, *Pichia* et *Saccharomyces*, et les champignons appartenant aux genres *Aspergillus*, *Penicillium* et *Rhizopus*.
- 35 3. Utilisation selon la revendication 1 ou 2, pour laquelle la protéine capable de s'ancrer dans la paroi cellulaire est choisie dans l'ensemble comprenant l'AGA1 (= α-agglutinine) de *S. cerevisiae*, le FLO1 (= protéine de flocation), la protéine majeure de paroi cellulaire des eucaryotes inférieurs choisis dans l'ensemble comprenant les levures et les champignons.
- 40 4. Utilisation selon l'une quelconque des revendications 1 à 3, pour laquelle la protéine assurant l'activité catalytique est choisie dans l'ensemble comprenant les enzymes hydrolytiques, parmi lesquelles les lipases, et les oxydoréductases, parmi lesquelles les oxydases.
- 45 5. Utilisation selon la revendication 1, pour laquelle ledit eucaryote inférieur comprend en outre une séquence codant pour un peptide signal assurant la sécrétion du produit d'expression dudit premier polynucléotide.
- 50 6. Utilisation selon la revendication 5, pour laquelle la protéine assurant l'activité catalytique présente ladite activité catalytique quand elle est présente sous une forme multimère, ledit eucaryote inférieur comprenant en outre un deuxième polynucléotide comprenant un gène de structure codant pour la même protéine assurant l'activité catalytique, en combinaison avec une séquence codant pour un peptide signal assurant la sécrétion du produit d'expression dudit deuxième polynucléotide, ledit deuxième polynucléotide étant lié d'une manière opérationnelle à un promoteur régulable.

Patentansprüche

1. Verwendung eines niederen Eukaryoten, ausgewählt aus der Gruppe, die aus Hefen und Pilzen besteht, enthaltend ein exprimierbares erstes Polynucleotid, umfassend ein Struktur-Gen, das ein Protein mit katalytischer Aktivität kodiert, wobei das Protein im Außenbereich der Zellwand des niederen Eukaryoten immobilisiert ist, und mindestens ein Teil eines Gens, kodierend für ein Ankerprotein, das zum Verankern in der Zellwand des niederen Eukaryoten fähig ist, wobei der Teil zumindest den Ankerteil des Ankerproteins kodiert, wobei der Ankerteil aus der C-terminalen Hälfte des Ankerproteins ableitbar ist, wobei das erste Polynucleotid entweder in einem Vektor oder in einem Chromosom des niederen Eukaryoten vorliegt, zum Durchführen eines enzymatischen Verfahrens, in dem ein Substrat für das die katalytische Aktivität aufweisende Protein mit dem niederen Eukaryoten in Kontakt gebracht wird.
2. Verwendung gemäß Anspruch 1, wobei der niedere Eukaryot aus der Gruppe ausgewählt ist, die aus Hefen besteht, die zu den Genera *Candida*, *Debaryomyces*, *Hansenula*, *Kluyveromyces*, *Pichia* und *Saccharomyces* gehört, und Pilze verwendet werden können, die zu den Genera *Aspergillus*, *Penicillium* und *Rhizopus* gehören.
3. Verwendung gemäß Anspruch 1 oder 2, wobei das zur Verankerung in der Zellwand fähige Protein aus der Gruppe ausgewählt ist, die besteht aus: AGA1 (=α-Agglutinin) von *S. cerevisiae*, FLO1 (=Flokkulationsprotein), Major-Carbohydrate-Binding-Protein von niederen Eukaryoten, ausgewählt aus der Gruppe, die aus Hefen und Pilzen besteht.
4. Verwendung gemäß mindestens einem der Ansprüche 1 bis 3, wobei das eine katalytische Aktivität bereitstellende Protein aus der Gruppe ausgewählt ist, die aus hydrolytischen Enzymen, einschließlich Lipasen, und Oxidoreduktasen, einschließlich Oxidasen, besteht.
5. Verwendung gemäß Anspruch 1, wobei der niedere Eukaryot darüber hinaus eine Sequenz umfasst, die ein Signalpeptid kodiert, das die Sekretion des Expressionsproduktes des ersten Polynucleotids sicherstellt.
6. Verwendung gemäß Anspruch 5, wobei das die katalytische Aktivität bereitstellende Protein die katalytische Aktivität zeigt, wenn es in multimerer Form vorliegt, wobei der niedere Eukaryot darüber hinaus ein zweites Polynucleotid umfasst, umfassend ein Struktur-Gen, das das gleiche Protein mit katalytischer Aktivität in Kombination mit einer Sequenz kodiert, die für ein Signalpeptid kodiert, das die Sekretion des Expressionsproduktes des Polynucleotids sicherstellt, wobei das zweite Polynucleotid operabel mit einem regulierbaren Promotor verbunden ist.

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FIGURE 1,

DNA SEQUENCE OF ALPHA-AGGLUTENIN:

1 AAGCTTTAGG TAAGGGAGGC AGGGGGAAAA GATACTGAAA
 41 TGACGGAAAA CGAGAATATG GAGCAGGGAG CAACCTTTAG
 81 AGCTTTACCC GTTAAAAGGT CAAATCGAGG CTTCCCTGCCT
 121 TTGTCTGATT TTAGTAGTAC CGGAAGGTTT ATTACGCCA
 161 AGAACAGTGC TTGAATTGAG TTCTCGGGAC ACGGGAAAGA
 201 CAATGGAAGA AAAATTACA TTCAGTAGCC TTATATATGA
 241 AATGCTGCCA AGCCACGTCT TTATAAGTAG ATAATGTCCC
 281 ATGAGCTGAA CTATGGGAAT TTATGACGCA GTTCATTGTA
 321 TATATATTAC ATTAACTCTT TAGTTAAACA TCTGAATTGT
 361 TTTATAAAAT AACTTTTGA ATTTTTTAT GATCGCTTAG
 401 TTAAGTCTAT TATATCAGGT TTTTCATTTC ATCATAATTG
 441 TTCGTTAAAT ATGAGTATAT TTAAATACAG GAATTAGTAT
 481 CATTGCACT CACGAAAAGG GCCGTTTCAT AGAGAGTTT
 521 CTTAATAAAAG TTGAGGGTTT CCGTGATAGT TTTGAGGGT
 561 TGTGGAACG AGATTACGC TTACCTTCAT ACTGATTAAT
 601 TTTTCAGCG GGCTTATCAT AATCATCCAT CATAGCAGTC
 641 TTTCTGGACT TCGTCGAGGA CTGGCTTCT GAATTTGAC
 681 GGTCCCTATT AGCTCCAGTT GGAGGAATTG AGTTACCTAC
 721 AACTGGCAAG AGGTCTTGT TTGGATTCAA AATAGGACTT
 761 TGTGGTAGCA GTTGGTTTT ATTCAATCTA AAGATATGAG
 801 AAACAGGTTT TAAGTAAATC GATACTATTG TACCAATGTT
 841 TAGCTCCAAT TCCTCCAAAA CGGTGGGATC TAATTTGTG
 881 TTCATTCTA TTAGTGGCAA CTCTCCGTCC AGTACTGATT
 921 TTAAAGATTG AAAAGTTATC GCGTTTGATA TACGAGACGT
 961 TTTCGTTAAT GACAGCAATC TCCAATACAT CAGTGGTTA
 1001 TCTCTTAAGT CAGGATTATT TTCGTGATCG GTGCATCCTT
 1041 TTAATAAAATC CATAACAAAGT TCTTCAGTTT CCTTTGTAGG
 1081 ATTCTGATG AAGAATTAA TTGCTGAGTT CAGAATGGAA
 1121 AATTGCACTT CTAGCGTCTC ATTAAACATG TTTGAGGAAA
 1161 AAACTCTAAA TAACTCCAGG TAGTTGGAA TTACATCCGA
 1201 ATATTGCGTT ATTATCCAGA TCATAGCGTT TTTGATTCA
 1241 GGTCCTGTA CAACTTCAGT GTGTTGACT AGTTCTGTTA
 1281 CGTTGCTTT AAAATTATTG GGATATTCC TCAAAATATT
 1321 TCTGAAAACC GAAATAATCT CCTGGACGAC ATAATCAACA
 1361 CCGAATTCTA ACAAAATCTAG TAGCACAGCG ACACAATCGT
 1401 GTACAGAGTC TTCATCTAGC TTAACAGCGA GATTACCAAT
 1441 GGCTCTGACT GATTTCTTG ACATTTGAAT ATCAATATCT
 1481 GTAGCATATT GTTCCAACTC TTCTAGAATT CTTGGTAATG
 1521 TTTCCCTTGTT AGCTAAAAGA TATAAACACT CTAATTCGT
 1561 GTCTTGATG TATATGGGGT CATTGTACTC GATGAAAAAA

FIGURE 1,

1601 TACGAAATGT CTAGCCTGAG TAGAGATGAC TCCCTACTCA
 1641 ATAAAAGAAG AATAACGTTT CTTAATACTA AAAATTGTAA
 1681 TTCAGGCGGC TTATCTAAC AAGCTATTAC AGAGTTAGAT
 1721 AGCTTTCCG CTAGAGTTTC TTTGATGACG TCAACATAAT
 1761 TCAACAAGTA CATGATGAAT TTTAAAGAGT TCAACACTAC
 1801 GTATGTGTT ACTTGTTGCA GGTACGGTAA AGCTAGTTCG
 1841 ATCATTTCAT GGGTATCCAA ATAATGCTGC GGCACAAACG
 1881 AAGTCGTCAA AACTTCCAAA ACAGTAGCCT TATTCCACTC
 1921 ATTTAATTG TGAAAGGT CTAGCATGTC AAAAGCGAGT
 1961 TCCAAGGGAA TCCTGAAGGT TCCATGTTAG CGTTTTTTTC
 2001 GTGAATGGAA TATAAAGTAT GTAATGCAGC TACAATGACT
 2041 TCTGGAGAGC TCGACTGTGC CTTTACAATG TCATGTAGAA
 2081 TGCTTGATAAA CCCCAATACC CTTTCATGAT CAATTCATC
 2121 TAAATCCAAC AGTGCCTAAA TTGCTGTCCT CGTCACTTGT
 2161 TCAGGTGGAG ACTTGTGATT TACCAATGAA ATGATACAGT
 2201 CGAAGGCCTG ATCAGATAGC TCTTCACCG GGACTAAATAC
 2241 CAGAGTTCTT AGTGCCTTA TTTGTAACCT TTCATCTCTG
 2281 CTTTGAAAT CGTCCATTAT AAATGGAAA GCCTCTCTGG
 2321 CCTGCTGAGG TTTAATGCG CCGATCACCC TAATATACTC
 2361 ATGGCAAATT CTTTCACCT CTAGATCATC TTCAATTGCG
 2401 CAAAATTCA AGAGCTCAGA AAACAGAAGG GACATTCGC
 2441 CATAGTTCC TAGAACCAAA TTGGCGATAA TTTTCTCAG
 2481 AGCATTTC CTTCTGTTA TATTGATTT AAACTTTTT
 2521 ACTCCAAAAT GTTGCAGATC TGTGACGATT TCATTTGCTT
 2561 TATATCTGGC AAAAACTTT TGATCGGACA TAAGCGAAAT
 2601 ACGTCCTATT AATGAAGTGA ATGTTCTTGC TGTATTCCCT
 2641 TCTTGTGCAG TAGATTAATT CTGTTTCCAG GCTGCGATAC
 2681 TTTGATACCC AATACTAAAA GTTGATGATT TGAACGATCT
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 2801 GAGATCATGA TTAAGGAAAG GTAAGTGATA TGCATGAATG
 2841 GGAATAGGCT TTGAAACTTG ACGATTTAGT TCCTTATTTC
 2881 TATCCATCTA ATCCTCCAAC TTCAATAGGC CTTATCTAGC
 2921 TCAGAGCAGT ATTAAATTGA GAATAGTAGC TTAATTGAAA
 2961 CCTTACTAAA AAAGTGTATG GTTACATAAG ATAAGGCCTT
 3001 AAGAAGAGTA TACATATGCA TTATTGATTA CCAAGACCAC
 3041 TATGAATAGT AATACCATAT TTAGCTTTG AAACATCATGT
 3081 TTTCTATTGT GTTGTTCAA ATTCCCTCTGT TAGGCTCAAT
 3121 TTAGGTTAAT TAAATTATAA AAAATATAA AAAATAAAGA
 3161 AAGTTTATCC ATCGGCACCT CAATTCAATG GAGTAAACAG
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 3241 GTTCCCCGCC ACGAGGCAAG TGTAGGTCTT TTGTCCATT

FIGURE 1,

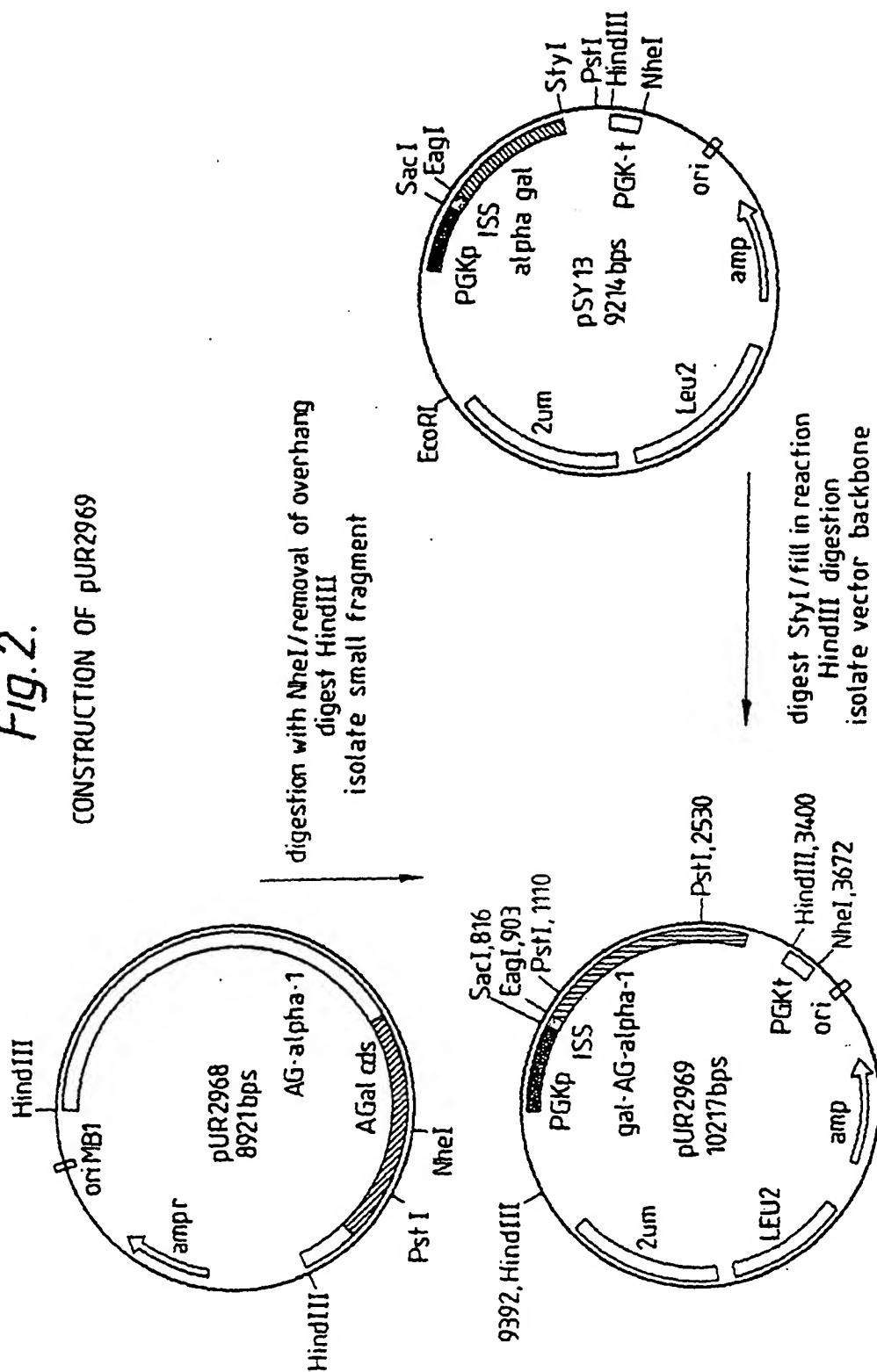
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 3401 ACTCATTCT TCAGTAACGG CGCTTAAATA TTCCCAAAAAA
 3441 CGTTACAATG GAATTGTTG ATCATGTAAC GAAATGCAAT
 3481 CTTCTAAAAA AAAAGCCATG TGAATCAAAA AAAGATTCT
 3521 TTTAGCATAc TATAAATATG CAAAATGCC C TCTATTATT
 3561 CTAGTAATCG TCCATTCTCA TATCTCCTT ATATCAGTCG
 3601 CCTCGCTTAA TATAGTCAGC ACAAAAGGAA CAACAATTG
 3641 CCAGTTTCA AAATGTTCAC TTTCTCAAA ATTATTCTGT
 3681 GGCTTTTTC CTTGGCATTG GCCTCTGCTA TAAATATCAA
 3721 CGATATCACA TTTCCAATT TAGAAATTAC TCCACTGACT
 3761 GCAAATAAAC AACCTGATCA AGGTTGGACT GCCACTTTG
 3801 ATTTAGTAT TGCAGATGCG TCTTCCATTA GGGAGGGCGA
 3841 TGAATTCAc TTATCAATGC CACATGTTA TAGGATTAAG
 3881 CTATTAAACT CATCGCAAAC AGCTACTATT TCCTTAGCGG
 3921 ATGGTACTGA GGCTTCAAA TGCTATGTT CGCAACAGGC
 3961 TGCATACTTG TATGAAAATA CTACTTCAC ATGTACTGCT
 4001 CAAAATGACC TGTCTCCTA TAATACGATT GATGGATCCA
 4041 TAACATTTTC GCTAAATTG AGTGTGGTG GTTCCAGCTA
 4081 TGAATATGAG TTAGAAAACG CTAAGTTTT CAAATCTGGG
 4121 CCAATGCTTG TTAAACTTGG TAATCAAATG TCAGATGTGG
 4161 TGAATTCGA TCCTGCTGCT TTTACAGAGA ATGTTTTCA
 4201 CTCTGGCGT TCAACTGGTT ACGGTTCTTT TGAAAGTTAT
 4241 CATTGGGTA TGTATTGTCC AAACGGATAT TTCCTGGGTG
 4281 GTACTGAGAA GATTGATTAC GACAGTTCCA ATAACAATGT
 4321 CGATTGGAT TGTTCTTCAG TTCAGGTTA TTCATCCAAT
 4361 GATTTAATG ATTGGTGGTT CCCGAAAGT TACAATGATA
 4401 CCAATGCTGA CGTCACTTGT TTTGGTAGTA ATCTGTGGAT
 4441 TACACTTGAC GAAAAACTAT ATGATGGGGA AATGTTATGG
 4481 GTTAATGCAT TACAATCTCT ACCCGCTAAT GTAAACACAA
 4521 TAGATCATGC GTTAGAATT CAATACACAT GCCTTGATAC
 4561 CATAGCAAAT ACTACGTACG CTACGCAATT CTCGACTACT
 4601 AGGGAATTAA TTGTTTATCA GGGTCGGAAC CTCGGTACAG
 4641 CTAGGCCAA AAGCTTTT ATCTCAACCA CTACTACTGA
 4681 TTTAACAAAGT ATAAACACTA GTGCGTATTC CACTGGATCC
 4721 ATTTCCACAG TAGAAACAGG CAATCGAACT ACATCAGAAG
 4761 TGATCAGTCA TGTTGGTACT ACCAGCACAA AACTGTCTCC
 4801 AACTGCTACT ACCAGCCTGA CAATTGCACA AACCAAGTATC
 4841 TATTCTACTG ACTCAAATAT CACAGTAGGA ACAGATATTG
 4881 ACACCACATC AGAAGTGATT AGTGATGTGG AAACCATTAG
 4921 CAGAGAAACA GCTTCGACCG TTGTAGCCGC TCCAACCTCA

FIGURE 1,

4961 ACAACTGGAT GGACAGGCGC TATGAATACT TACATCCCGC
5001 AATTACATC CTCTTCTTTC GCAACAATCA ACAGCACACC
5041 AATAATCTCT TCATCAGCAG TATTGAAAC CTCAGATGCT
5081 TCAATTGTCA ATGTGCACAC TGAAAATATC ACGAATACTG
5121 CTGCTGTTCC ATCTGAAGAG CCCACTTTG TAAATGCCAC
5161 GAGAAACTCC TTAAATTCCCT TCTGCAGCAG CAAACAGCCA
5201 TCCAGTCCCT CATCTTATAC GTCTTCCCCA CTCGTATCGT
5241 CCCTCTCCGT AAGCAAACA TTACTAAGCA CCAGTTTAC
5281 GCCTTCTGTG CCAACATCTA ATACATATAT CAAAACGGAA
5321 AATACGGGTT ACTTTGAGCA CACGGCTTG ACAACATCTT
5361 CAGTTGGCCT TAATTCTTT AGTGAACAG CACTCTCATC
5401 TCAGGGAACG AAAATTGACA CCTTTTAGT GTCATCCTTG
5441 ATCGCATATC CTTCTCTGC ATCAGGAAGC CAATTGTCCG
5481 GTATCCAACA GAATTTACA TCAACTTCTC TCATGATTTC
5521 AACCTATGAA GGTAAAGCGT CTATATTTT CTCAGCTGAG
5561 CTCGGTTCGA TCATTTTCT GCTTTGTCG TACCTGCTAT
5601 TCTAAAACGG GTACTGTACA GTTAGTACAT TGAGTCGAAA
5641 TATAcgAAAT TATTGTTCAT AATTTTCATC CTGGCTCTT
5681 TTTCTTCAA CCATAGTTAA ATGGACAGTT CATATCTTAA
5721 ACTCTAATAA TACTTTCTA GTTCTTATCC TTTCCGTCT
5761 CACCGCAGAT TTTATCATAG TATTAAATT ATATTTGTT
5801 CGTAAAAAGA AAAATTGTG AGCGTTACCG CTCGTTCAT
5841 TACCCGAAGG CTGTTCACT AGACCACTGA TTAAGTAAGT
5881 AGATGAAAAA ATTCATCAC CATGAAAGAG TTGATGAGA
5921 GCTACTTTT CAAATGCTTA ACAGCTAACCC GCCATTCAAT
5961 AATGTTACGT TCTCTTCATT CTGCGGCTAC GTTATCTAAC
6001 AAGAGGTTT ACTCTCTCAT ATCTCATCA AATAGAAAGA
6041 ACATAATCAA AAAGCTT 6057

Fig. 2.

CONSTRUCTION OF pUR2969



ALPHA GALACTOSIDASE ACTIVITY MT302/1c WITH pSY13

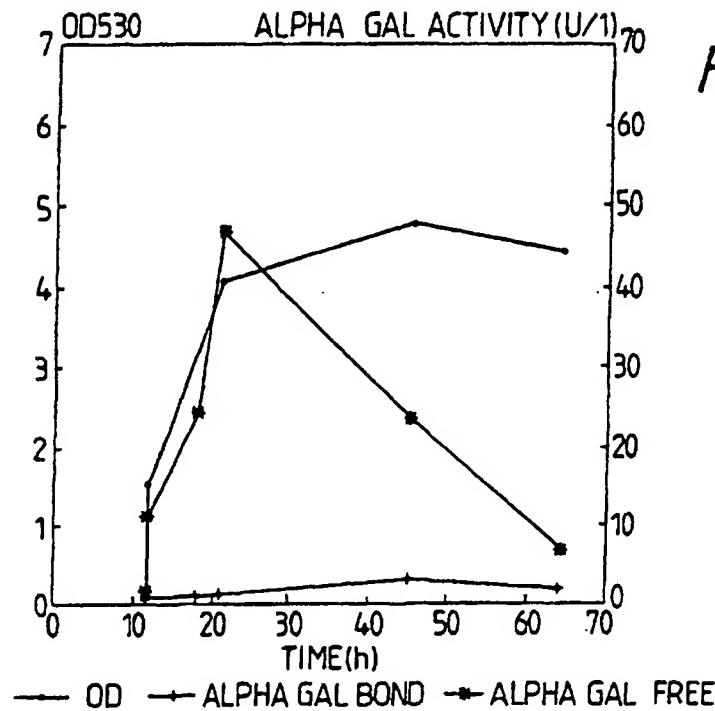


Fig. 3A

ALPHA GALACTOSIDASE ACTIVITY MT302/1c WITH pSY13

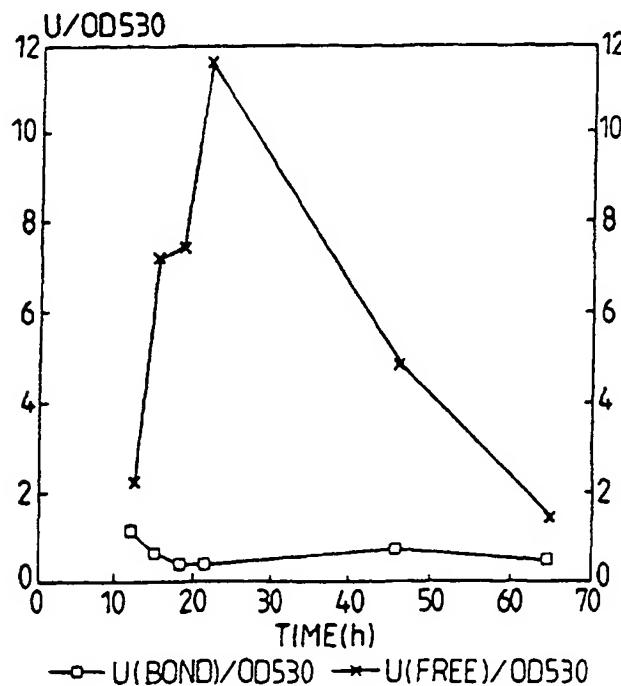


Fig. 3B

ALPHA GALACTOSIDASE ACTIVITY MT302/1c WITH pUR2969

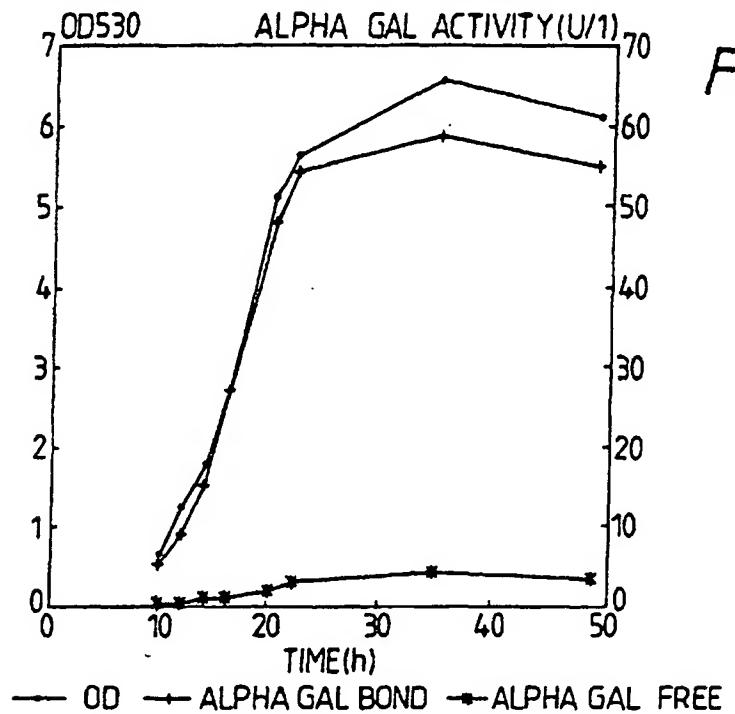


Fig. 4A

ALPHA GALACTOSIDASE ACTIVITY MT302/1c WITH pUR2969

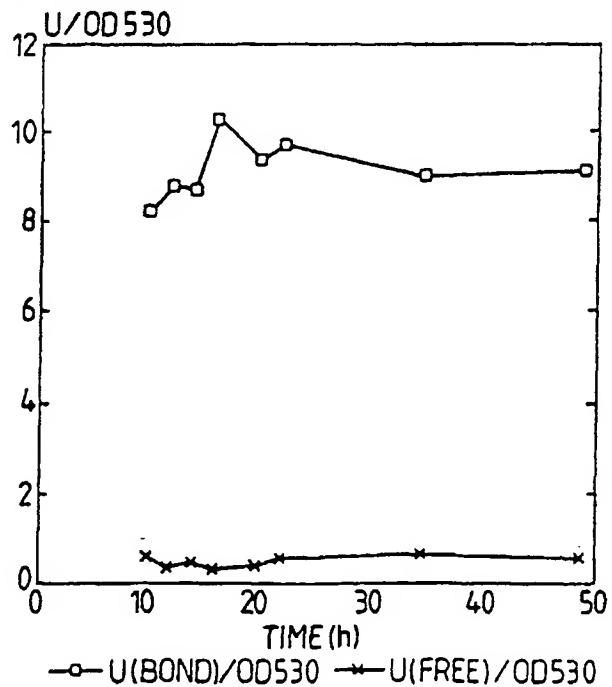


Fig. 4B

Fig. 5.

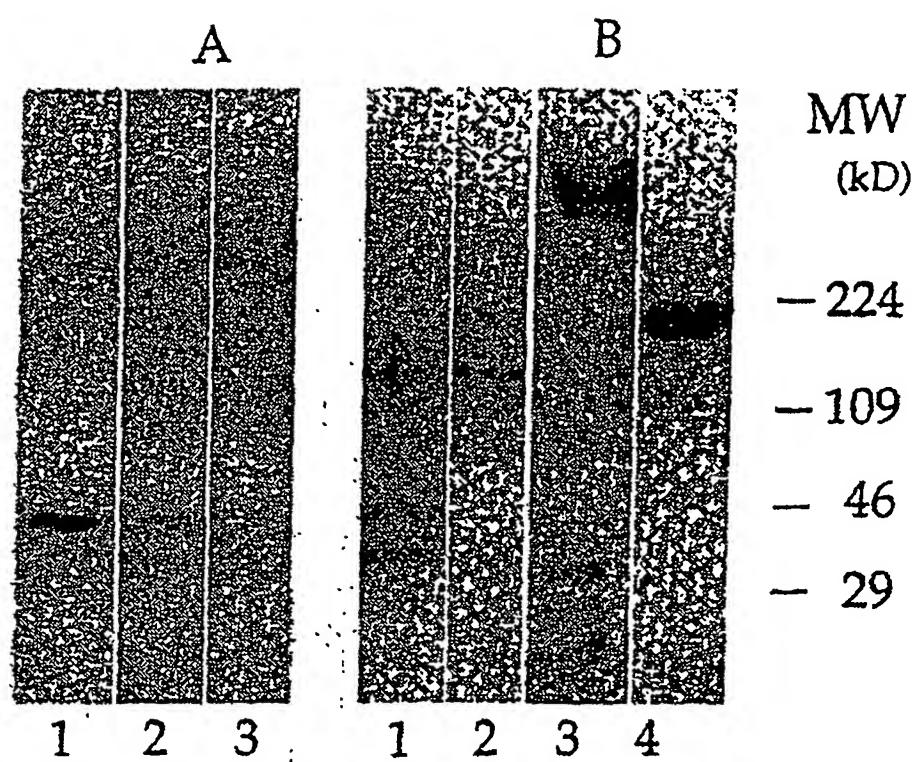
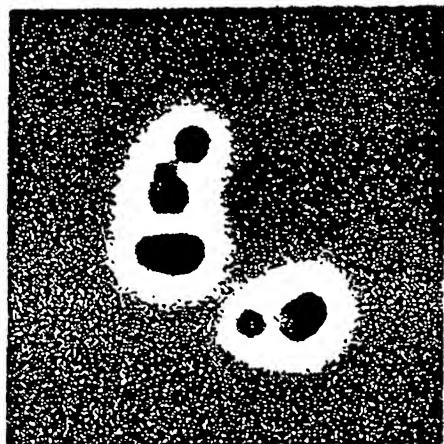
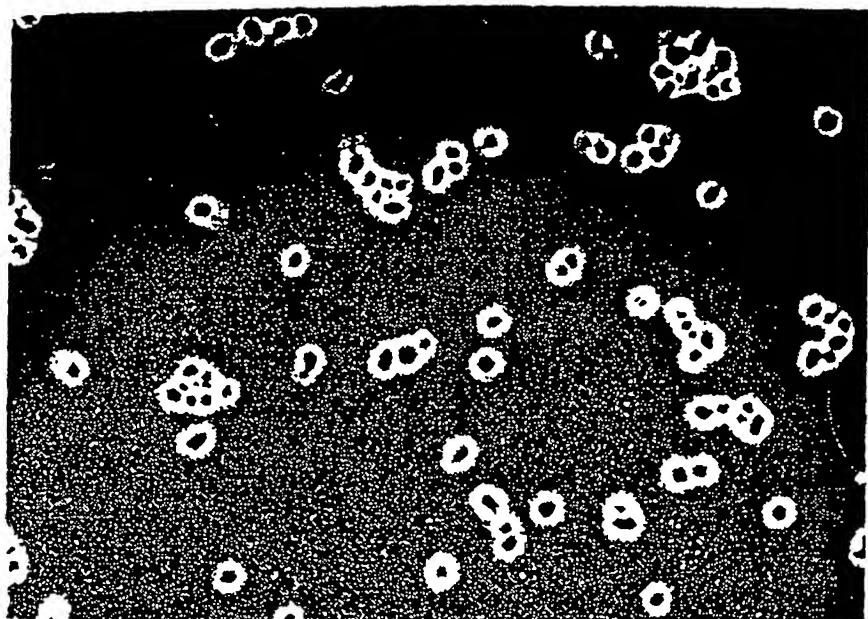


Fig. 6. (1/2)



(2/2)

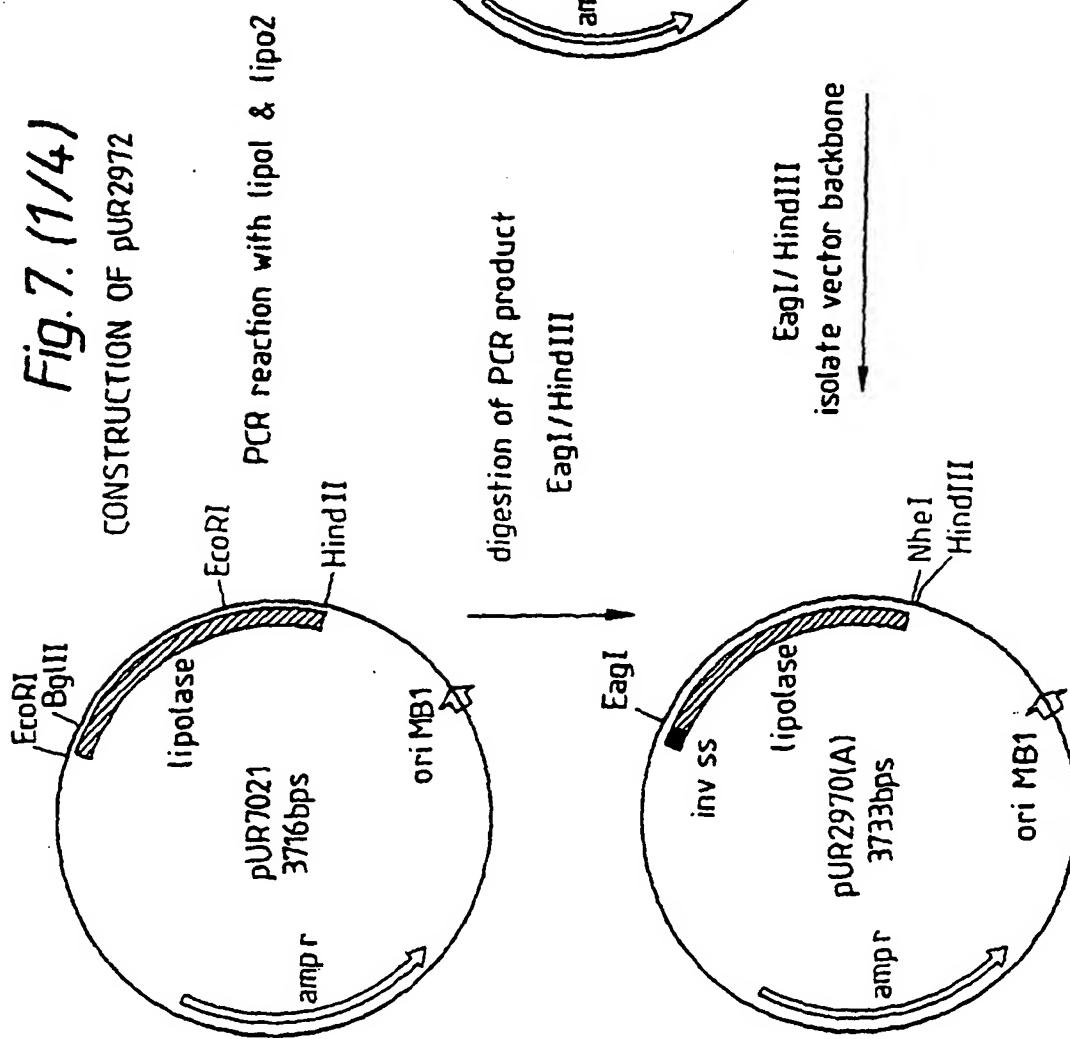


Fig. 7 (2/4)

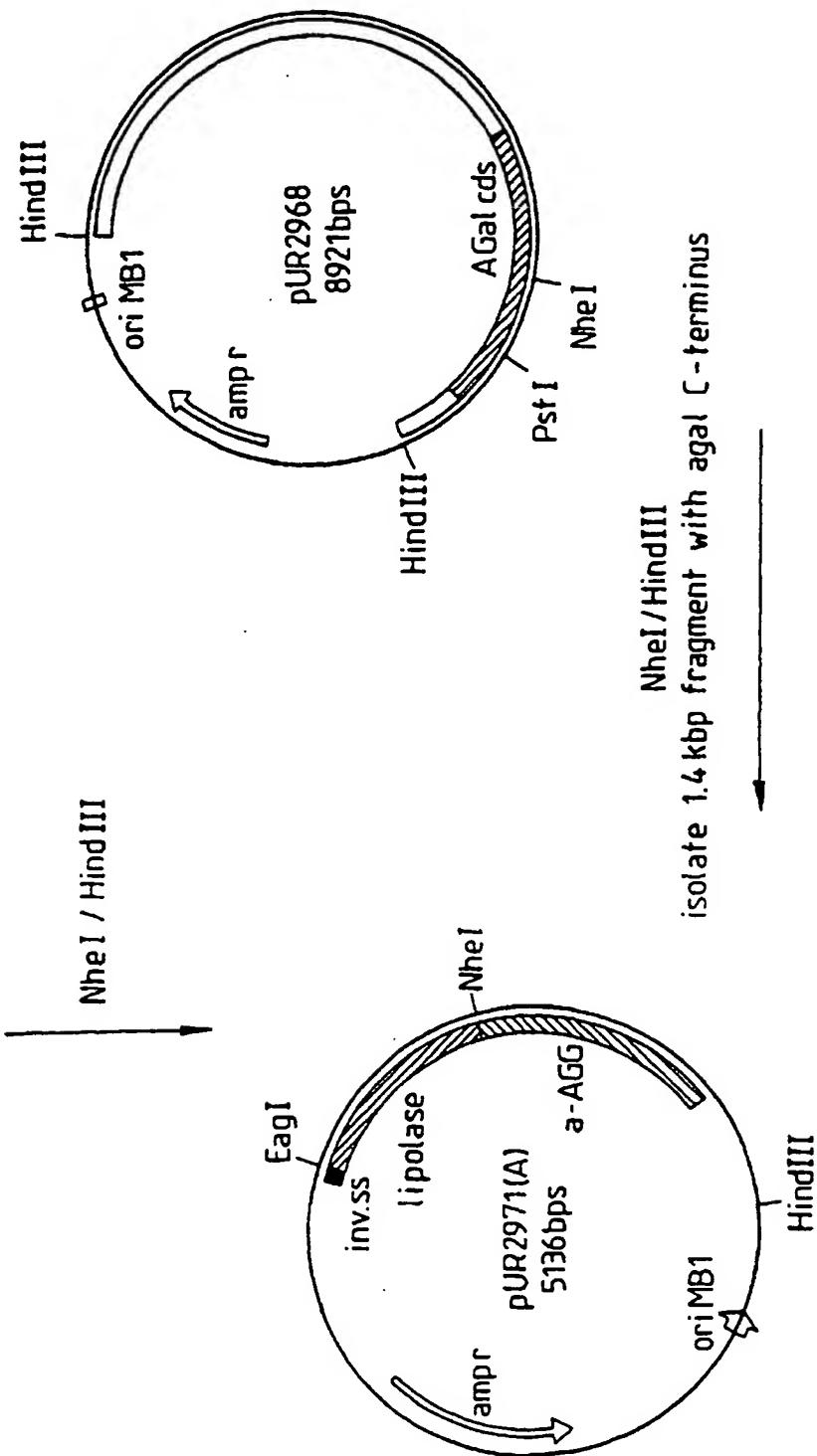


Fig. 7 (3/4)

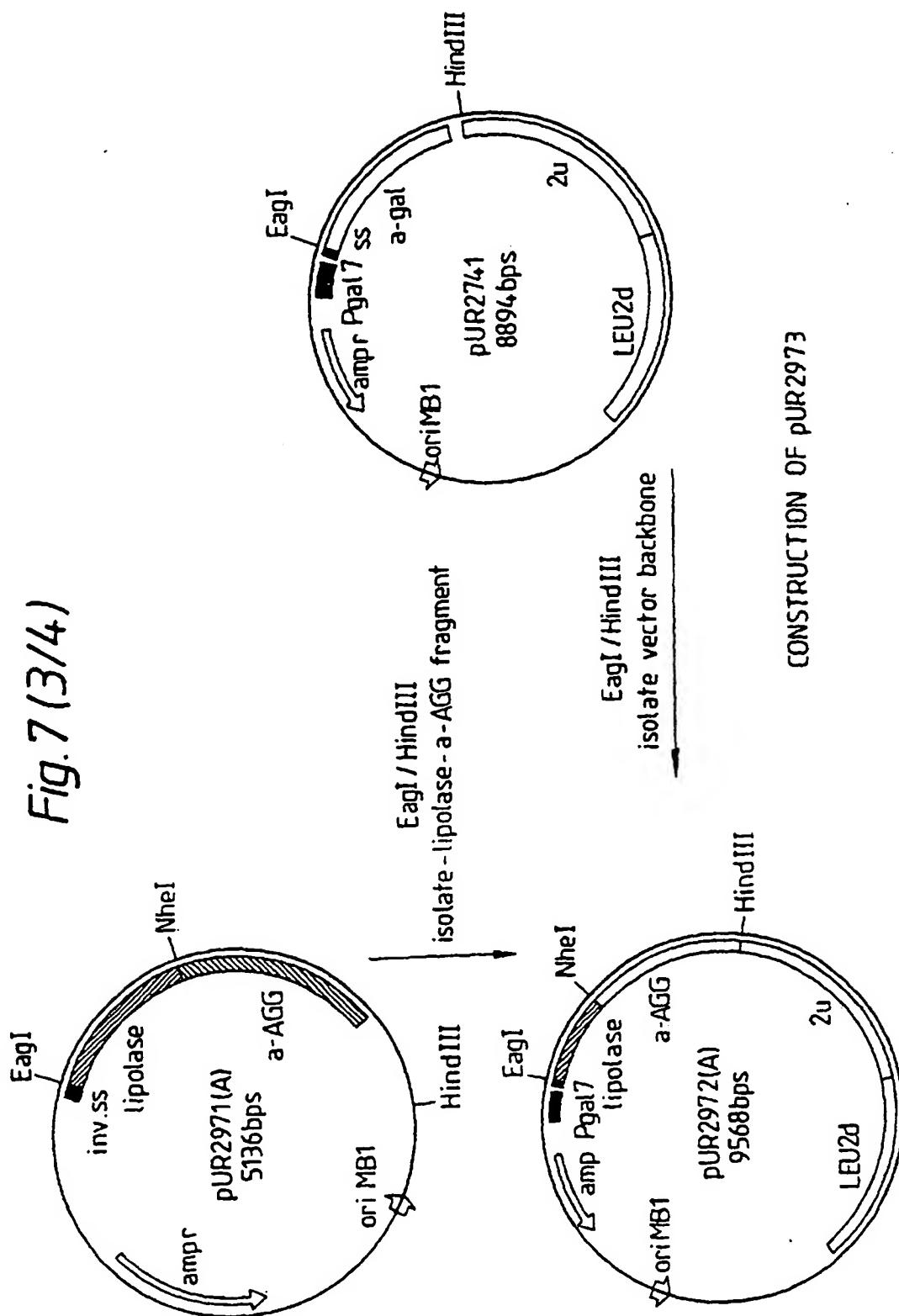


Fig. 7 (4/4)

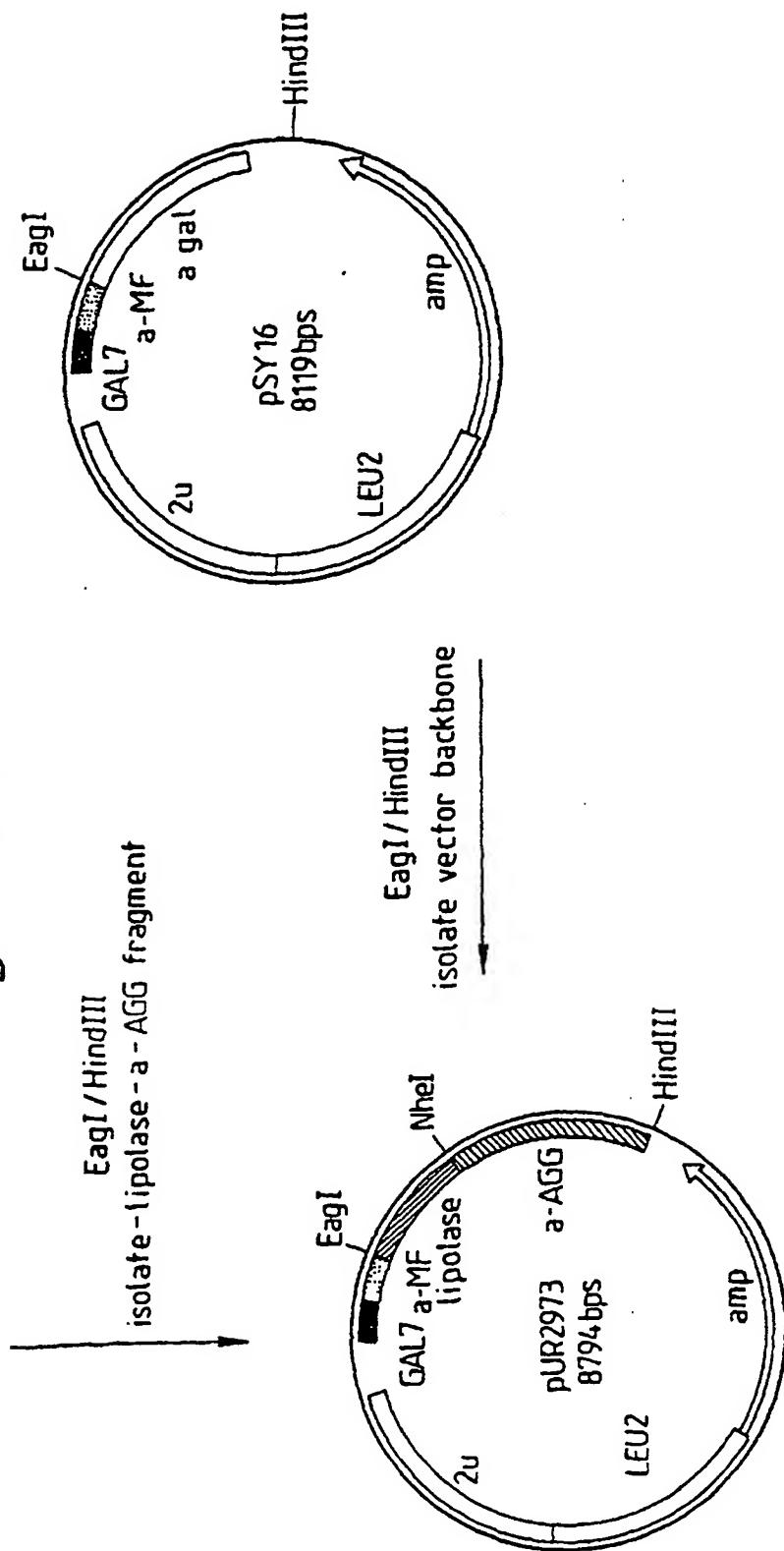


FIGURE 8,

DNA SEQUENCE OF LIPASE B:

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1 AATTGGCAC GAGATTCTT TGATTTCAA CTGTTAATCA
41 TGGTTTCAA AAGCTTTTT TTGGCTGCGG CGCTAACGT
81 AGTGGGCACC TTGGCCCAGG CCCCCACGGC CGTTCTTAAT
121 GGCAACGAGG TCATCTCTGG TGTCTTGAG GGCAAGGTTG
161 ATACCTCAA GGGAAATCCCA TTTGCTGACC CTCCTGTTGG
201 TGACTTGCGG TTCAAGCACC CCCAGCCTT CACTGGATCC
241 TACCAGGGTC TTAAGGCCAA CGACTTCAGC TCTGCTTGTA
281 TGCAGCTTGA TCCTGGCAAT GCCTTTCTT TGCTTGACAA
321 AGTAGTGGGC TTGGGAAAGA TTCTTCCTGA TAACCTTAGA
361 GGCCCTCTT ATGACATGGC CCAGGGTAGT GTCTCCATGA
401 ATGAGGACTG TCTCTACCTT AACGTTTCC GCCCCGCTGG
441 CACCAAGCCT GATGCTAACG TCCCCGTCAT GGTTGGATT
481 TACGGTGGTG CCTTTGTGTT TGTTCTTCT GCTTCTTACC
521 CTGGTAACGG CTACGTCAAG GAGAGTGTGG AAATGGGCCA
561 GCCTGTTGTG TTTGTTCCA TCAACTACCG TACCGGCCCC
601 TATGGATTCT TGGGTGGTGA TGCCATCACC GCTGAGGGCA
641 ACACCAACGC TGGTCTGCAC GACCAGCGCA AGGGTCTCGA
681 GTGGGTTAGC GACAACATTG CCAACTTGG TGGTGATCCC
721 GACAAGGTCA TGATTTCGG TGAGTCCGCT GGTGCCATGA
761 GTGTTGCTCA CCAGCTTGTG GCCTACGGTG GTGACAACAC
801 CTACAACGGA AAGCAGCTT TCCACTCTGC CATTCTTCAG
841 TCTGGCGGTG CTCTTCCTA CTTTGACTCT ACTTCTGTTG
881 GTCCCGAGAG TGCCTACAGC AGATTTGCTC AGTATGCCGG
921 ATGTGACACC AGTGCCAGTG ATAATGACAC TCTGGTTGT
961 CTCCGCAGCA AGTCCAGCGA TGTCTTGAC AGTGCAGCAGA
1001 ACTCGTATGA TCTTAAGGAC CTGTTGGTC TGCTCCCTCA
1041 ATTCTTGGA TTTGGTCCA GACCCGACGG CAACATTATT
1081 CCCGATGCCG CTTATGAGCT CTACCGCAGC GGTAGATAACG
1121 CCAAGGTTCC CTACATTACT GGCAACCAGG AGGATGAGGG
1161 TACTATTCTT GCCCCCCGTG CTATTAATGC TACCACTACT
1201 CCCCATGTTA AGAAGTGGTT GAAAGTACATT TGTAGCCAGG
1241 CTTCTGACGC TTGCTTGAT CGTGTGTTGT CGCTCTACCC
1281 CGGCTCTTGG TCGGAGGGTT CACCATTCCG CACTGGTATT
1321 CTTAATGCTC TTACCCCTCA GTCAAGCGC ATTGCTGCCA
1361 TTTCACTGA TTTGCTGTT CAGTCTCCTC GTCGTGTTAT
1401 GCTTAACGCT ACCAAGGACG TCAACCGCTG GACTTACCTT
1441 GCCACCCAGC TCCATAACCT CGTTCCATT TTGGGTACTT
1481 TCCATGGCAG TGATCTTCTT TTTCAATACT ACGTGGACCT
1521 TGGCCCATCT TCTGCTTACC GCGCTACTT TATCTCGTTT
1561 GCCAACCAAC ACGACCCCAA CGTTGGTACC AACCTCCAAC

```

FIGURE 8,

1601 AGTGGGATAT GTACACTGAT GCAGGCAAGG AGATGCTTCA
1641 GATTCATATG ATTGGTAACT CTATGAGAAC TGACGACTTT
1681 AGAATCGAGG GAATCTCGAA CTTTGAGTCT GACGTTACTC
1721 TCTTCGGTTA ATCCCATTAA GCAAGTTTG TGTATTCAA
1761 GTATACCAGT TGATGTAATA TATCAATAGA TTACAAATTA
1801 ATTAGTGAAA AAAAAAAAAA AAAAAAAAC 1828

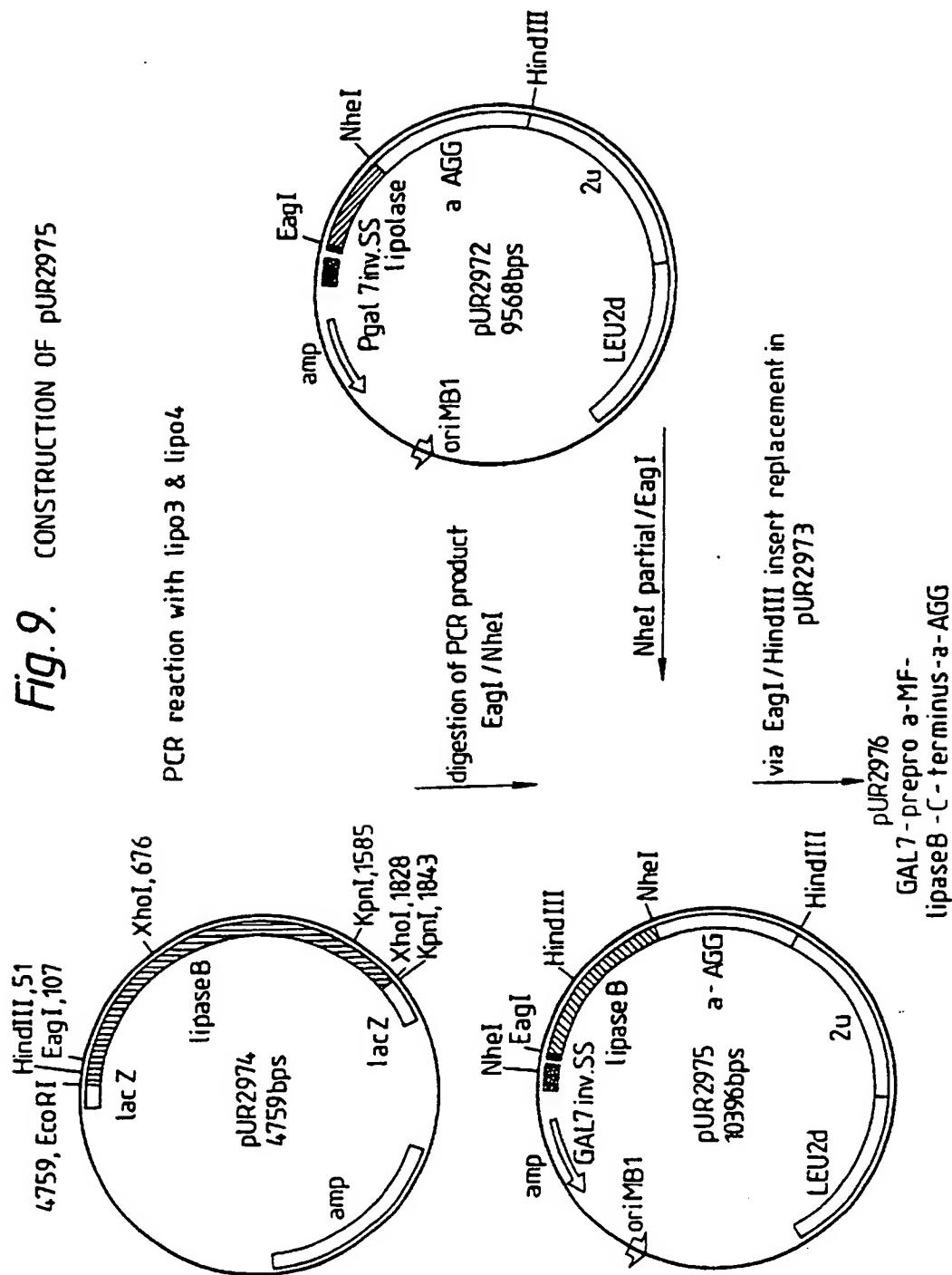
Fig. 9. CONSTRUCTION OF PUR2975

Fig.10 (1/2) CONSTRUCTION OF pUR2981

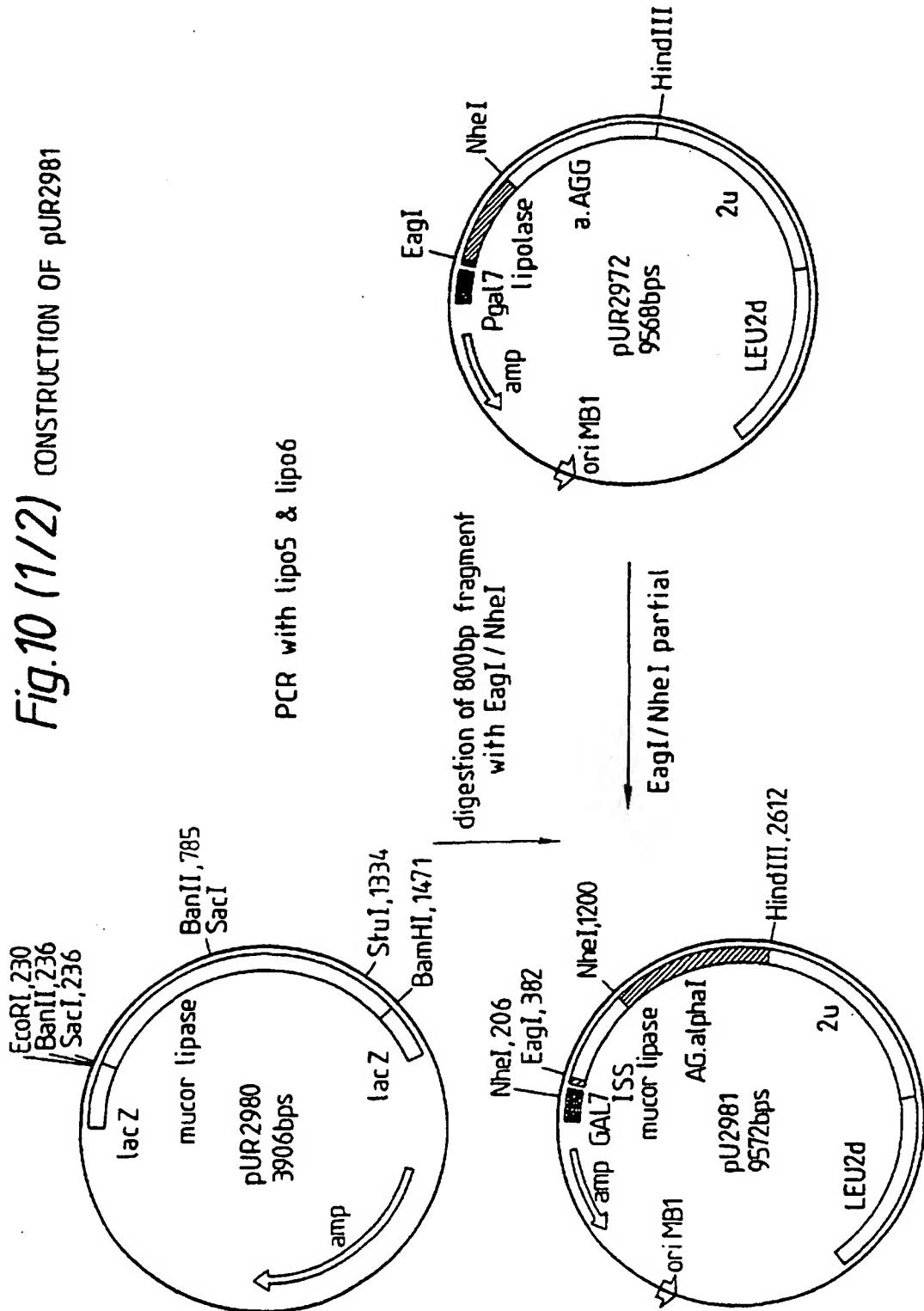


Fig.10 (2/2) CONSTRUCTION OF PUR2982

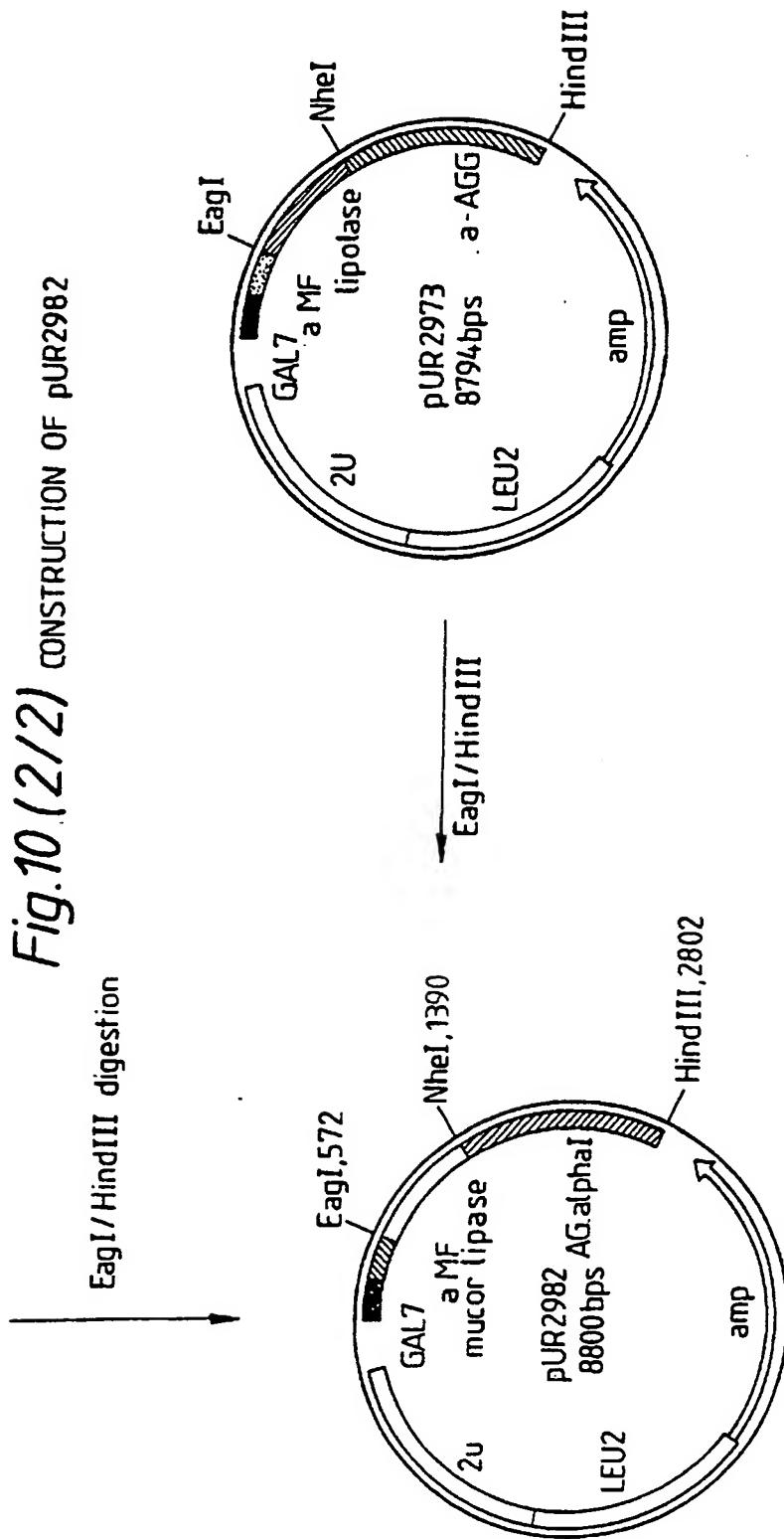


FIGURE 11,

DNA SEQUENCE OF FLO1:

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1 ATGACAATGC CTCATCGCTA TATGTTTTG GCAGTCTTA
41 CACTTCTGGC ACTAACTAGT GTGGCCTCAG GAGCCACAGA
81 GGC GTGCTTA CCAGCAGGCC AGAGGAAAAG TGGGATGAAT
121 ATA AATTTTT ACCAGTATTG ATTGAAAGAT TCCTCCACAT
161 ATT CGAATGC AGCATATAATG GCTTATGGAT ATGCCTCAAA
201 AACCAA ACTA GGTTCTGTG GAGGACAAAC TGATATCTCG
241 ATT GATTATA ATATTCCCTG TGTTAGTTCA TCAGGCACAT
281 TTC CTTGTCC TCAAGAAGAT TCCTATGGAA ACTGGGGATG
321 CAAAGGAATG GGTGCTTGTG CTAATAGTCA AGGAATTGCA
361 TACTGGAGTA CTGATTATT TGTTTTCTAT ACTACCCCAA
401 CAAACGTAAAC CCTAGAAATG ACAGGTTATT TTTTACCACC
441 ACAGACGGGT TCTTACACAT TCAAGTTGC TACAGTTGAC
481 GACTCTGCAA TTCTATCAGT AGGTGGTGCA ACCGCGTTCA
521 ACT GTTGTGC TCAACAGCAA CCGCCGATCA CATCAACGAA
561 CTTTACCAATT GACGGTATCA AGCCATGGGG TGGAAAGTTG
601 CCACCTAATA TCGAAGGAAC CGTCTATATG TACGCTGGCT
641 ACT ATTATATCC AATGAAGGTT GTTACTCGA ACGCTGTTTC
681 TTGGGGTACA CTTCCAATTG GTGTGACACT TCCAGATGGT
721 ACCACTGTAA GTGATGACTT CGAAGGGTAC GTCTATTCT
761 TTGACGATGA CCTAAGTCAA TCTAACTGTA CTGTCCCTGA
801 CCCTTCAAAT TATGCTGTCA GTACCACTAC AACTACAACG
841 GAACCATGGA CCGGTACTTT CACTTCTACA TCTACTGAAA
881 TGACCACC GT CACCGGTACC AACGGCGTTC CAACTGACGA
921 AACCGTCATT GTCATCAGAA CTCCAACCAG TGAAGGTCTA
961 ATCAGCACCA CCACTGAACC ATGGACTGGC ACTTTCACTT
1001 CGACTTCCAC TGAGGTTACC ACCATCACTG GAACCAACGG
1041 TCAACCAACT GACGAAACTG TGATTGTTAT CAGAACTCCA
1081 ACCAGTGAAG GTCTAACAG CACCACCACT GAACCATGGA
1121 CTGGTACTTT CACTTCTACA TCTACTGAAA TGACCACCGT
1161 CACCGGTACT AACGGTCAAC CAACTGACGA AACCGTGATT
1201 GTTATCAGAA CTCCAACCAG TGAAGGTTTG GTTACAACCA
1241 CCACTGAACC ATGGACTGGT ACTTTTACTT CGACTTCCAC
1281 TGAAATGTCT ACTGTCACTG GAACCAATGG CTTGCCAACT
1321 GATGAAACTG TCATTGTTGT CAAA ACTTCCA ACTACTGCCA
1361 TCTCATCCAG TTTGTCA TCATCTTCAG GACAAATCAC
1401 CAGCTCTATC ACGTCTTCGC GTCCAATTAT TACCCCATTC
1441 TATCCTAGCA ATGGAACCTTC TGTGATTTCT TCCTCAGTAA
1481 TTTCTTCCTC AGTCACTTCT TCTCTATTCA CTTCTTCTCC
1521 AGTCATTCTC TCCTCAGTCA TTTCTTCTTC TACAACAAACC
1561 TCCACTTCTA TATTTCTGA ATCATCTAAA TCATCCGTCA

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FIGURE 11,

1601 TTCCAACCAG TAGTTCCACC TCTGGTTCTT CTGAGAGCGA
 1641 AACGAGTTCA GCTGGTTCTG TCTCTTCTTC CTCTTTATC
 1681 TCTTCTGAAT CATCAAAATC TCCTACATAT TCTTCTTCAT
 1721 CATTACCACT TGTTACCACT GCGACAACAA GCCAGGAAAC
 1761 TGCTTCTTCA TTACCACCTG CTACCACTAC AAAAACGAGC
 1801 GAACAAACCA CTTGGTTAC CGTGACATCC TGCGAGTCTC
 1841 ATGTGTGCAC TGAATCCATC TCCCCTGCGA TTGTTCCAC
 1881 AGCTACTGTT ACTGTTAGCG GCGTCACAAC AGAGTATAAC
 1921 ACATGGTGCC CTATTCTAC TACAGAGACA ACAAAGCAAA
 1961 CCAAAGGGAC AACAGAGCAA ACCACAGAAA CAACAAAACA
 2001 AACCAACGGTA GTTACAATT CTTCTTGTA ATCTGACGTA
 2041 TGCTCTAAGA CTGCTTCTCC AGCCATTGTA TCTACAAGCA
 2081 CTGCTACTAT TAACGGCGTT ACTACAGAAT ACACAAACATG
 2121 GTGTCCTATT TCCACCACAG AATCGAGGCA ACAAAACAACG
 2161 CTAGTTACTG TTACTTCCTG CGAATCTGGT GTGTGTTCCG
 2201 AAACTGCTTC ACCTGCCATT GTTTCGACGG CCACGGCTAC
 2241 TGTGAATGAT GTTGGTACGG TCTATCCTAC ATGGAGGCCA
 2281 CAGACTGCGA ATGAAGAGTC TGTCAGCTCT AAAATGAACA
 2321 GTGCTACCGG TGAGACAACA ACCAATACTT TAGCTGCTGA
 2361 AACGACTTACCA AATACTGTAG CTGCTGAGAC GATTACCAAT
 2401 ACTGGAGCTG CTGAGACGAA AACAGTAGTC ACCTCTTCGC
 2441 TTTCAAGATC TAATCACGCT GAAACACAGA CGGCTTCCGC
 2481 GACCGATGTG ATTGGTCACA GCAGTAGTGT TGTTCTGTA
 2521 TCCGAAACTG GCAACACCAA GAGTCTAACCA AGTTCCGGGT
 2561 TGAGTACTAT GTCGCAACAG CCTCGTAGCA CACCAGCAAG
 2601 CAGCATGGTA GGATATAGTA CAGCTTCTT AGAAATTCA
 2641 ACGTATGCTG GCAGTGCAAC AGCTTACTGG CCGGTAGTGG
 2681 TTTAA 2685

Fig. 12.
CONSTRUCTION OF pUR2990

PCR with oligonucleotides pcrflo1 & pcrflo2
Isolate 1950 bp fragment
cut with NheI and HindIII
ligate into HindIII/ NheI (p) digested pUR2972

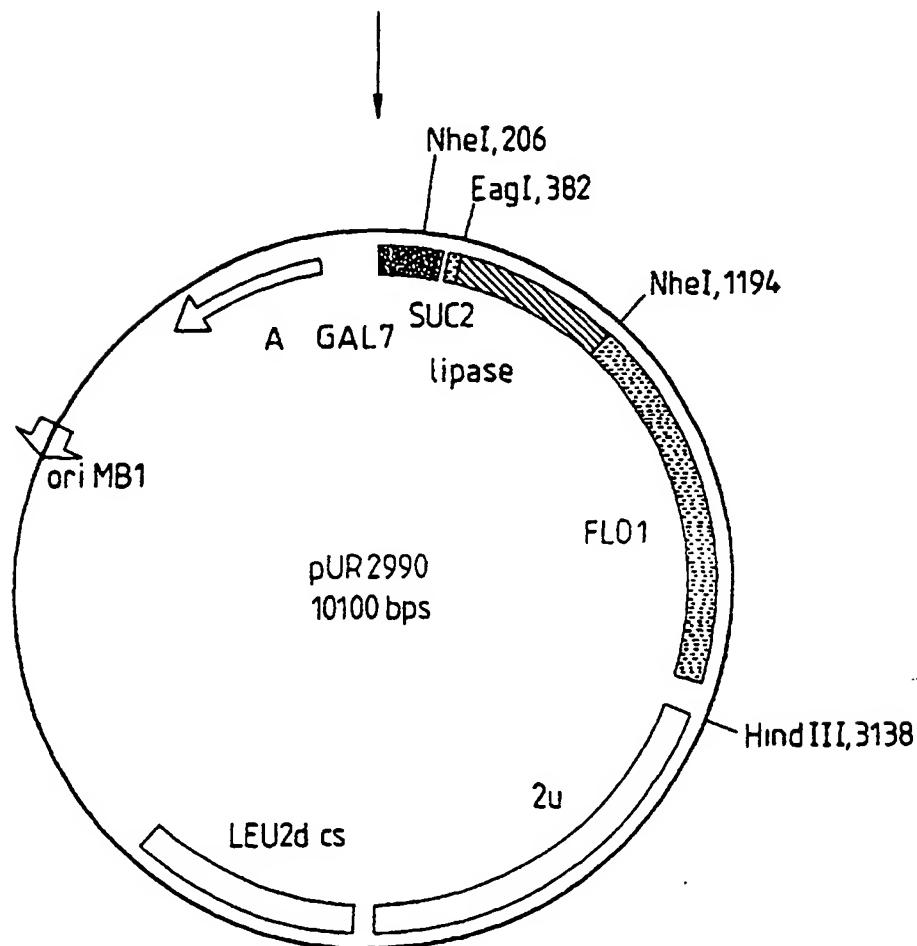


Fig. 13.

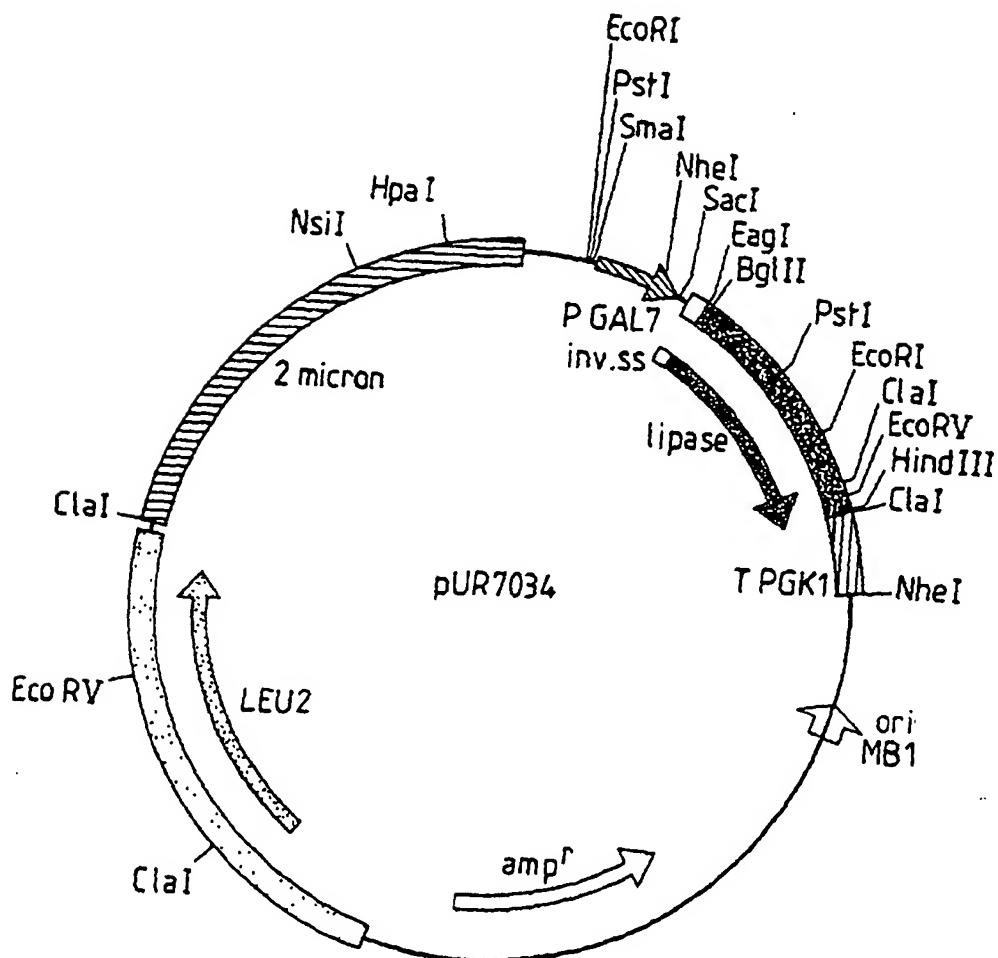


Fig.14.

